

GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: August 5, 2004, 13:28:09 ; Search time 54 Seconds
(without alignments)
2103.409 Million cell updates/sec

Title: US-10-018-257A-2
Perfect score: 2133
Sequence: 1 MDKLDANVSEEGFGSVKX.....ESQCHPPATSPILVAQPSDT 402

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database: A_Geneseq_29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1980s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	426	4	AAB59572 Human 5-HT4
2	2069	97.0	402	4	AAB59573 Dog 5-HT4
3	2042	95.7	388	6	ADA83842 Human HTR
4	2042	95.7	388	6	ADA83841 Human HTR
5	2042	95.7	388	6	AAO19909 Human TA4
6	2042	95.7	388	6	ABB99742 Amino aci
7	2042	95.7	388	6	ABP81768 Human 5-HT
8	2037	95.5	388	4	ABB56323 Non-endog
9	2014	94.4	388	2	AAR57032 Serotonin
10	1954	91.6	388	6	AAO19905 Human TA4
11	1879	88.1	406	2	AAR57030 Rat 5-HT4
12	1878	88.0	360	2	AAV14522 Human ser
13	1877	88.0	380	2	AAV14521 Human ser
14	1874	87.9	387	4	ABB56322 Non-endog
15	1873	87.8	360	4	ABB56325 Non-endog
16	1872	87.8	380	4	ABB56324 Non-endog
17	1869.5	87.6	378	4	ABB56326 Non-endog
18	1755	82.3	387	2	AAR57029 Rat 5-HT4
19	1239	58.1	261	2	AAV14522 Human ser
20	919	43.1	178	2	AAR57033 Serotonin
21	598.5	28.1	508	4	ABB56327
22	598.5	28.1	508	4	AAU38945
23	598.5	28.1	508	7	ADC35817 Drosophil
24	582.5	27.3	446	2	AAR15498 Human dop
25	582.5	27.3	446	2	AAR38364 Human dop

26	582.5	27.3	446	4	ABB56347
27	582.5	27.3	446	6	ABP81807 Human dop
28	582.5	27.3	446	7	ADC86175 Human GPC
29	577	27.1	382	5	ABG75676 Human DIA
30	575	27.0	447	7	ADD26057 Human dop
31	567.5	26.6	446	2	AAR15499 Rat dopam
32	567.5	26.6	446	6	ABM04785 Rat dopam
33	566	26.5	418	2	AAR30501 N-termina
34	565.5	26.5	477	2	AAR21082 Dopamine
35	564.5	26.5	757	2	AAR30497 N-termina
36	563.5	26.4	477	4	ABB56350 Non-endog
37	563.5	26.4	477	6	ABP81808 Human dop
38	562.5	26.4	475	2	AAR31046 Rat DIB d
39	562.5	26.4	487	2	AAW09795 D1 dopami
40	561.5	26.3	477	2	AAR79381 Dopamine
41	561.5	26.3	477	2	AAW40802 Human D5
42	561	26.3	428	2	AAR13729 Human bet
43	559.5	26.2	370	5	ABG75674 Human bet
44	559.5	26.2	415	2	AAW44932 Canine be
45	555.5	26.0	487	2	AAR13596 D1 dopami

ALIGNMENTS

RESULT 1
AAB59572
ID AAB59572 standard; protein; 426 AA.
XX
AC AAB59572;
XX
AC AAB59572;
XX
23-MAR-2001 (first entry)
XX
Human 5-HT4(h) receptor splice variant.
DE
Human: 5-HT4(h) receptor; 5-hydroxytryptamine; HT; serotonin;
KW Oesophageal disorder; asthma; bronchitis; pneumonia;
KW Irritable bowel syndrome; cancer; cytostatic; antidiabetic;
KW Antiinflammatory; vulnery; antisense gene therapy.
XX
Homo sapiens.
XX
WO200077199-A1.
XX
21-DEC-2000.
XX
14-JUN-2000; 2000WO-EP005592.
XX
14-JUN-1999; 99GB-00013850.
XX
(JANC) JANSSEN PHARM NV.
XX
Bender E, Pindon AN, Van Oers IP, Jurzak M, Luyten WHML;
WPI; 2001-071270/08.
XX
N-PSDB; AAR23986.
XX
Novel human 5-HT4 receptor splice variant useful for treating heartburn,
PT reflux, esophagitis, Barrett's esophagus, esophageal cancer, achalasia,
PT esophageal stenosis and esophageal spasms.
XX
Claim 19; Fig 1B; 64pp; English.

The present sequence is the human 5-hydroxytryptamine (HT)4(h) (serotonin) receptor protein. The protein is useful as a medicament for treating heartburn, reflux, oesophagitis, Barrett's oesophagus, oesophageal cancer, achalasia, oesophageal stenosis, oesophageal spasms, oesophageal hiatal hernia or other oesophageal motility disorders, and its oesophageal irritation, such as asthma, bronchospasms, aspiration, and its consequences (bronchitis, bronchial pneumonia, bronchiectasia) and other diseases of the lower oesophageal sphincter, irritable bowel syndrome, denervation of the oesophagus (e.g. after certain types of trauma or surgery), and disturbances in oesophageal innervation. It is useful for

[illegible]

R	19-FEB-2002; 2002US-0357144P.	ID	ADAB3841 standard; protein; 388 AA.
X	(BIOM-) BIOMEDICAL CENT.	XX	
A		AC	ADAB3841;
I	Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;	XX	
X	WPI; 2003-175241/17.	DT	20-NOV-2003 (first entry)
R	N-PSDB; ADAB3840.	DE	Human HTR45 protein.
X		XX	
X		KW	human; marker; expressed sequence tag; EST; arabidopsis; tumour;
T	Determining if a nucleic acid is a marker for a phenotype/cell type of	KW	stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
T	interest, by global comparison of expressed sequence tags known to be	XX	vaccine.
T	expressed in the phenotype/cell type with all ESTs expressed in normal	OS	Homo sapiens.
X	tissue.	XX	
S		PN	WO2002103028-A2.
X	Claim 29; Page 243-244; 516pp; English.	XX	
C	The invention relates to a novel method for determining if a nucleic acid	PD	27-DEC-2002.
C	is a marker for a predetermined phenotype/cell type of interest from a	XX	
C	biological species. The method comprises performing a global comparison	PF	30-MAY-2002; 2002WO-IB004189.
C	of a group of expressed sequence tags (ESTs) known to be expressed in the	XX	
C	phenotype/cell type of interest with all ESTs expressed in normal tissue	PR	30-MAY-2001; 2001US-0293999P.
C	in order to identify ESTs that are preferentially expressed in the	PR	22-OCT-2001; 2001US-0330457P.
C	phenotype/cell of interest. A method of the invention is useful for	PR	19-FEB-2002; 2002US-0357144P.
C	determining whether a nucleic acid is a marker for a predetermined	XX	(BIOM-) BIOMEDICAL CENT.
C	phenotype or cell type of interest from a biological species, preferably	PA	
C	Arabidopsis or human. The cell type of interest is an abnormal cell such	XX	
C	as a tumour cell, and the predetermined phenotype is a stress-induced	PI	
C	phenotype such as hyperosmotic stress or high salt conditions. A method	XX	
C	of the invention is also useful for determining the progression of colon	XX	
C	cancer in a human, for detecting a tumour cell, and for regulating or	DR	Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
C	preventing the growth of a tumour cell. An antibody of the invention is	DR	WPI; 2003-175241/17.
C	useful for detecting the absence or presence of peptides encoded by	XX	N-PSDB; ADAB3839.
C	tumour-associated markers. A polypeptide of the invention is useful as an	PT	
C	immunogen for vaccinating an animal. The present sequence represents a	PT	Determining if a nucleic acid is a marker for a phenotype/cell type of
C	tumour-associated antigen of the invention.	PT	interest, by global comparison of expressed sequence tags known to be
X		PT	expressed in the phenotype/cell type with all ESTs expressed in normal
X		PT	tissue.
Q	Sequence 388 AA;	XX	
		PS	Claim 29; Page 241-243; 516pp; English.
		XX	
		CC	The invention relates to a novel method for determining if a nucleic acid
		CC	is a marker for a predetermined phenotype/cell type of interest from a
		CC	biological species. The method comprises performing a global comparison
		CC	of a group of expressed sequence tags (ESTs) known to be expressed in the
		CC	phenotype/cell type of interest with all ESTs expressed in normal tissue
		CC	in order to identify ESTs that are preferentially expressed in the
		CC	phenotype/cell of interest. A method of the invention is useful for
		CC	determining whether a nucleic acid is a marker for a predetermined
		CC	phenotype or cell type of interest from a biological species, preferably
		CC	Arabidopsis or human. The cell type of interest is an abnormal cell such
		CC	as a tumour cell, and the predetermined phenotype is a stress-induced
		CC	phenotype such as hyperosmotic stress or high salt conditions. A method
		CC	of the invention is also useful for determining the progression of colon
		CC	cancer in a human, for detecting a tumour cell, and for regulating or
		CC	preventing the growth of a tumour cell. An antibody of the invention is
		CC	useful for detecting the absence or presence of peptides encoded by
		CC	tumour-associated markers. A polypeptide of the invention is useful as an
		CC	immunogen for vaccinating an animal. The present sequence represents a
		CC	tumour-associated antigen of the invention.
		XX	
		SQ	Sequence 388 AA;
			Query Match 95.7%; Score 2042; DB 6; Length 388;
			Best Local Similarity 96.5%; Pred. No. 2.9e-214;
			Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
Y	1 MDKLDANVSSEEGFGSVEKVLLTFLSTVILMAILGNLLVMVAVCDRLRKIKNYFIV 60	QY	1 MDKLDANVSSEEGFGSVEKVLLTFLSTVILMAILGNLLVMVAVCDRLRKIKNYFIV 60
b	1 MDKLDANVSSEEGFGSVEKVLLTFLSTVILMAILGNLLVMVAVCDRLRKIKNYFIV 60	Db	1 MDKLDANVSSEEGFGSVEKVLLTFLSTVILMAILGNLLVMVAVCDRLRKIKNYFIV 60
Y	61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDTRY 120	QY	61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDTRY 120
b	61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDTRY 120	Db	61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDTRY 120
Y	121 AICCPFLVYRNKMTPLRIALMLGGCWVPTFTSFLPIMQWNNIGIIDLSRLNQLGQD 180	QY	121 AICCPFLVYRNKMTPLRIALMLGGCWVPTFTSFLPIMQWNNIGIIDLSRLNQLGQD 180
b	121 AICCPFLVYRNKMTPLRIALMLGGCWVPTFTSFLPIMQWNNIGIIDLSRLNQLGQD 180		
Y	181 FHAIEKRKNQNSNTYCFVMNKPVAITCSVVAFYIPFLMWLAYRYIVTAKHAHQI 240		
b	170 ---IEKRKNQNSNTYCFVMNKPVAITCSVVAFYIPFLMWLAYRYIVTAKHAHQI 226		
Y	241 QMLQAGASSESPQSDQSHRMTETKAATLCIIMGCFLCWAPFVTVNVPFD 300		
b	227 QMLQAGASSESPQSDQSHRMTETKAATLCIIMGCFLCWAPFVTVNVPFD 286		
Y	301 YTVPGQVWTAFLWGLYINGSLNPLFLAFNLKSPRAFLIILCCDDRYRPRPSILGQTVPC 360		
b	287 YTVPGQVWTAFLWGLYINGSLNPLFLAFNLKSPRAFLIILCCDDRYRPRPSILGQTVPC 346		
Y	361 SITTINGSTHVLDAVECGQWESQCHPPATSPPLVAAQPSDT 402		
b	347 SITTINGSTHVLDAVECGQWESQCHPPATSPPLVAAQPSDT 388		
			RESULT 4
			DA83841

Db 121 AICCPQVYRNKMTPLRIALMLGGCWVPTFTSFLPIMQGNNGIIDL----- 169
 Qy 181 FFAIKRKNQNSNSTCYFVFNKPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 240
 Db 170 ---TEKRFKNQNSNSTCYFVFNKPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 226
 Qy 241 QMLORAGASSESRPQSDQHSRTHMETETKAATLCIIMCFCCLCWAPFFVTNVDPPID 300
 Db 227 QMLORAGASSESRPQSDQHSRTHMETETKAATLCIIMCFCCLCWAPFFVTNVDPPID 286
 Qy 301 YTVPGQVWTAFLMLGYINSLNPLFYAFLNKSFRRAFLIILCCDDERYRPSILGOTVPC 360
 Db 287 YTVPGQVWTAFLMLGYINSLNPLFYAFLNKSFRRAFLIILCCDDERYRPSILGOTVPC 346
 Qy 361 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQPSDT 402
 Db 347 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQPSDT 388

RESULT 5

AAO19909
 ID AAO19909 standard; protein; 388 AA.

AC AAO19909;

DT 11-AUG-2003 (first entry)

XX Human TA4 receptor expression assay probe protein.

DE Human; G-protein coupled receptor; TA4 receptor; receptor; cytostatic;
 KW haemostatic; antisthmatic; cardiant; antidiabetic; anorectic; asthma;
 KW neuroprotective; haematological disorder; COPD; cardiovascular disease;
 KW CNS disorder; diabetes; obesity; cancer; genito-urinary disorder; probe.

OS Homo sapiens.

XX WO2002101043-A2.

XX 19-DEC-2002.

XX 06-JUN-2002; 2002WO-EP006204.

XX 08-JUN-2001; 2001US-0296447P.

XX 15-NOV-2001; 2001US-0331393P.

XX 17-APR-2002; 2002US-0372811P.

XX (FARB) BAYER AG.

XX Zhu Z;

XX WPI; 2003-148906/14.

XX Novel polynucleotide encoding G-protein coupled receptor, TA4 receptor,
 PT useful for treating hematological disorders, asthma, cardiovascular
 PT disorders, diabetes, obesity, cancer and genito-urinary disorders.

PS Example 18; Page 138-139; 144pp; English.

XX The present invention provides the protein and coding sequences of human
 CC TA4 receptor, which is a G-protein coupled receptor. The sequences are
 CC useful in the treatment of hematological disorders, chronic obstructive
 CC pulmonary disease, asthma, cardiovascular disorders, central nervous
 CC system (CNS) disorders, diabetes, obesity, cancer and genito-urinary
 CC disorders. The present sequence is a probe protein used to determine the
 CC expression levels of the human TA4 receptor protein

XX Sequence 388 AA;

Query Match 95.7%; Score 2042; DB 6; Length 388;
 Best Local Similarity 96.5%; Pred. No. 2.9e-214;
 Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Qy 1 MDKLDANVSSBEGFSGVEKVVLLTFLSTVILMALILGNLLVMVAVCWDRQLRKIKTNYFIV 60
 Db 1 MDKLDANVSSBEGFSGVEKVVLLTFLSTVILMALILGNLLVMVAVCWDRQLRKIKTNYFIV 60
 Qy 61 SLAPADLLSVLVNMPFGAIELVDQIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRIY 120
 Db 61 SLAPADLLSVLVNMPFGAIELVDQIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRIY 120
 Qy 121 AICCPQVYRNKMTPLRIALMLGGCWVPTFTSFLPIMQGNNGIIDLERSLQGLQD 180
 Db 121 AICCPQVYRNKMTPLRIALMLGGCWVPTFTSFLPIMQGNNGIIDL----- 169
 Qy 181 FFAIKRKNQNSNSTCYFVFNKPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 240
 Db 170 ---TEKRFKNQNSNSTCYFVFNKPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 226
 Qy 241 QMLORAGASSESRPQSDQHSRTHMETETKAATLCIIMCFCCLCWAPFFVTNVDPPID 300
 Db 227 QMLORAGASSESRPQSDQHSRTHMETETKAATLCIIMCFCCLCWAPFFVTNVDPPID 286
 Qy 301 YTVPGQVWTAFLMLGYINSLNPLFYAFLNKSFRRAFLIILCCDDERYRPSILGOTVPC 360
 Db 287 YTVPGQVWTAFLMLGYINSLNPLFYAFLNKSFRRAFLIILCCDDERYRPSILGOTVPC 346
 Qy 361 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQPSDT 402
 Db 347 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQPSDT 388

RESULT 6

ABB99742

ID ABB99742 standard; protein; 388 AA.

XX ABB99742;

XX 24-MAR-2003 (first entry)

XX Amino acid sequence of a protein 31% identical to human TAS receptor.

DE Human; trace amine receptor; TAS receptor; G protein-coupled receptor;
 KW GPCR; chromosome 6; haematological disorder; CNS disorder; asthma;
 KW chronic obstructive pulmonary disease; COPD; cardiovascular disorder;
 KW gastrointestinal disorder; cancer; diabetes; obesity;
 KW genitourinary disorder.

XX Homo sapiens.

XX WO200299107-A2.

XX 12-DEC-2002.

XX 06-JUN-2002; 2002WO-EP006206.

XX 07-JUN-2001; 2001US-0296136P.

XX 17-APR-2002; 2002US-0372809P.

XX (FARB) BAYER AG.

XX Zhu Z;

XX WPI; 2003-140624/13.

XX New polynucleotide encoding a G protein-coupled receptor polypeptide
 PT useful for treating diseases, e.g. hematological, cardiovascular,
 PT gastrointestinal or genitourinary disorders, asthma, cancer, diabetes,
 PT obesity.

PS Disclosure; Fig 4; 154pp; English.

XX The present sequence represents a protein which is 31% identical to a
 CC human trace amine receptor designated TAS receptor. TAS is a G protein-
 CC coupled receptor (GPCR), located on chromosome 6. TAS polypeptides and
 CC polynucleotides are useful for the preparation of a medicament for

C modulating the activity of the GPCR in a disease, e.g. haematological disorders, a CNS disorder, chronic obstructive pulmonary disease (COPD),
 C asthma, a cardiovascular disorder, a gastrointestinal disorder, cancer,
 C diabetes, obesity or genitourinary disorder
 X
 Q Sequence 388 AA;

Query Match 95.7%; Score 2042; DB 6; Length 388;
 Best Local Similarity 96.5%; Pred. No. 2.9e-214;
 Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 Y 1 MDKLDANVSSEEGFSGVEKVLTLFTSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
 b 1 MDKLDANVSSEEGFSGVEKVLTLFTSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
 Y 61 SLAFADLLVSVLWMPFGAIELVDQIMYIGVFCLVRLTSLDVLTTASIFHLCCISLDRIY 120
 b 61 SLAFADLLVSVLWMPFGAIELVDQIMYIGVFCLVRLTSLDVLTTASIFHLCCISLDRIY 120
 Y 121 AICCPVLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNOGLQD 180
 b 121 AICCPVLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNOGLQD 180
 Y 181 FPAIEKRFQNSNSTYCVFVNKPATITCSVAVFYIPFLMWLAYRYIVTAKHAHQI 240
 b 170 ---IEKRFQNSNSTYCVFVNKPATITCSVAVFYIPFLMWLAYRYIVTAKHAHQI 226
 Y 241 QMLQAGASSESPQADQHSRTHRTETKAAKTLCIMGCFCLWAPFVTNIVDPFID 300
 b 227 QMLQAGASSESPQADQHSRTHRTETKAAKTLCIMGCFCLWAPFVTNIVDPFID 286
 Y 301 YTVPGQVWTAFLWLGYNISGLNPFYAFLNKSPRAFLIILCCDDERYRRPSILQGVPC 360
 b 287 YTVPGQVWTAFLWLGYNISGLNPFYAFLNKSPRAFLIILCCDDERYRRPSILQGVPC 346
 Y 361 SITTINGSTHVLDAVECGQWESQCHPPATSPVAAPSDT 402
 b 347 SITTINGSTHVLDAVECGQWESQCHPPATSPVAAPSDT 388

RESULT 7
 BP81768
 D ABP81768 standard; protein; 388 AA.
 X
 C ABP81768;
 T
 T
 X 04-MAR-2003 (first entry)
 X 'Human 5-HT4 receptor protein SEQ ID NO:18.
 X G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 W G protein-coupled receptor modulator; antibody; immune-related disease;
 W growth-related disease; cell regeneration-related disease; AIDS; cancer;
 W immunological-related cell proliferative disease; autoimmune disease;
 W Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 W osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 W graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 W psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 W mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 W hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 W ulcer.
 X
 X Homo sapiens.
 S
 S WO200261087-A2.
 N
 X
 D 08-AUG-2002.
 X
 F 19-DEC-2001; 2001WO-US050107.
 X
 R 19-DEC-2000; 2000US-0257144P.
 X
 X (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;
 PT WPI; 2003-046718/04.
 XX N-PSDB; AB242612.
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242859 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 388 AA;

Query Match 95.7%; Score 2042; DB 6; Length 388;
 Best Local Similarity 96.5%; Pred. No. 2.9e-214;
 Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 QY 1 MDKLDANVSSEEGFSGVEKVLTLFTSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
 Db 1 MDKLDANVSSEEGFSGVEKVLTLFTSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
 QY 61 SLAFADLLVSVLWMPFGAIELVDQIMYIGVFCLVRLTSLDVLTTASIFHLCCISLDRIY 120
 Db 61 SLAFADLLVSVLWMPFGAIELVDQIMYIGVFCLVRLTSLDVLTTASIFHLCCISLDRIY 120
 QY 121 AICCPVLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNOGLQD 180
 Db 121 AICCPVLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNOGLQD 180
 QY 181 FPAIEKRFQNSNSTYCVFVNKPATITCSVAVFYIPFLMWLAYRYIVTAKHAHQI 240
 Db 170 ---IEKRFQNSNSTYCVFVNKPATITCSVAVFYIPFLMWLAYRYIVTAKHAHQI 226
 QY 241 QMLQAGASSESPQADQHSRTHRTETKAAKTLCIMGCFCLWAPFVTNIVDPFID 300
 Db 227 QMLQAGASSESPQADQHSRTHRTETKAAKTLCIMGCFCLWAPFVTNIVDPFID 286
 QY 301 YTVPGQVWTAFLWLGYNISGLNPFYAFLNKSPRAFLIILCCDDERYRRPSILQGVPC 360
 Db 287 YTVPGQVWTAFLWLGYNISGLNPFYAFLNKSPRAFLIILCCDDERYRRPSILQGVPC 346
 QY 361 SITTINGSTHVLDAVECGQWESQCHPPATSPVAAPSDT 402
 Db 347 SITTINGSTHVLDAVECGQWESQCHPPATSPVAAPSDT 388

RESULT 8
 ABB56323
 ID ABB56323 standard; protein; 388 AA.
 XX
 AC ABB56323;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Non-endogenous human GPCR protein, SEQ ID NO: 439.
 XX
 DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WC20017172-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX
 XX 05-APR-2001; 2001WO-US011098.
 PF
 XX
 XX 07-APR-2000; 2000US-0195747P.
 PR
 XX (AREN-) ARENA PHARM INC.
 PA
 XX
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;
 PI
 XX
 DR WPI; 2001-648759/74.
 DR N-PSDB; ABI97959.
 DR
 XX
 PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.
 PT
 XX
 PS Claim 1; Page 240-242; 394pp; English.
 XX
 CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR
 XX
 SQ Sequence 388 AA;
 Query Match 95.5%; Score 2037; DB 4; Length 388;
 Best Local Similarity 96.3%; Pred. No. 1e-213; 1; Indels 14; Gaps 1;
 Matches 387; Conservative 0; Mismatches 1;
 QY 1 MDKLDANVSSEEGFGSVEKVLTLFLSTVILMAILGNLVMVAVCWDRQLRKIKTYFIV 60
 DB 1 MDKLDANVSSEEGFGSVEKVLTLFLSTVILMAILGNLVMVAVCWDRQLRKIKTYFIV 60
 QY 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDLVLTASIFHLCCISLDYY 120
 DB 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDLVLTASIFHLCCISLDYY 120
 QY 121 AICCPOLVYRNKMTPLRIALMLGCGWVPTFISFLPIMOQWNNIGIIDLERSLNQGLQD 180
 DB 121 AICCPOLVYRNKMTPLRIALMLGCGWVPTFISFLPIMOQWNNIGIIDLERSLNQGLQD 180
 QY 181 FFAIRKKNQNSNSTCYFVMNKPVAITCSVVAFYIPFLMVLAYRYIVYTAKEHAQI 240
 DB 170 ---IEKKKNQNSNSTCYFVMNKPVAITCSVVAFYIPFLMVLAYRYIVYTAKEHAQI 226
 QY 241 QMLORAGASSESPQSDQHSRTHMETETKAKTLCIIMGCFCGLWAPFVTVNDPFD 300
 DB 227 QMLORAGASSESPQSDQHSRTHMETETKAKTLCIIMGCFCGLWAPFVTVNDPFD 286
 QY 301 YTVPGQWTAFLWGLYNSGLNPFYAFLNKSPRAFLIILCDDERYRRPSILGQTVPC 360

Db 287 YTVPGQWTAFLWGLYNSGLNPFYAFLNKSPRAFLIILCDDERYRRPSILGQTVPC 346
 QY 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 402
 DB 347 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 388
 RESULT 9
 AAR57032
 ID AAR57032 standard; protein; 388 AA.
 XX
 AC AAR57032;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAR-1995 (first entry)
 XX
 DE Serotonin receptor encoded by full-length human serotonin S10 clone.
 XX
 KW 5-HT4 serotonin receptor; 5-HT4R; 5-HT4A; adenylate cyclase; agonist;
 KW S10 clone.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO9414957-A2.
 PD 07-JUL-1994.
 XX
 XX 22-DEC-1993; 93WO-US012586.
 PF
 XX 24-DEC-1992; 92US-00996772.
 PR
 XX (SYNA-) SYNAPTIC PHARM CORP.
 PA
 XX
 PI Gerald C, Hartig P, Branchek TA, Weinshank RL;
 DR WPI; 1994-234695/28.
 DR N-PSDB; AAQ68831.
 DR
 XX Mammalian 5-HT4 serotonin receptor, corresp. DNA, probes, anti-sense
 PT oligo:nucleotide(s) and antibodies - useful for treating conditions
 PT involving abnormal 5-HT4 receptor expression, for screening for
 PT (ant)agonists, prodn. of transgenic animals etc.
 PS Example; Page 96-98; 161pp; English.
 XX
 CC S10 is a 270 bp fragment identified when rat brain cDNA was used as
 CC template in a PCR with the degenerate primers 3.17 (AAQ68832) and 5.5
 CC (AAQ68833). The clone represents a potentially new serotonin receptor. By
 CC direct PCR analysis of bacterial pools, sib selection and filter
 CC hybridisation, two full-length cDNA clones - S10-87, 5.5kb; and S10-95,
 CC 4.5kb - were determined. The full length human S10 clones are given in
 CC AAQ68831 and AAR57032. Page 11 describes these sequences as clone S10-95
 CC and page 96 describes them as clone S10-87. (Updated on 25-MAR-2003 to
 CC correct EN field.)
 XX
 SQ Sequence 388 AA;
 Query Match 94.4%; Score 2014; DB 2; Length 388;
 Best Local Similarity 95.0%; Pred. No. 3.3e-211;
 Matches 382; Conservative 3; Mismatches 3; Indels 14; Gaps 1;
 QY 1 MDKLDANVSSEEGFGSVEKVLTLFLSTVILMAILGNLVMVAVCWDRQLRKIKTYFIV 60
 DB 1 MDKLDANVSSEEGFGSVEKVLTLFLSTVILMAILGNLVMVAVCWDRQLRKIKTYFIV 60
 QY 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDLVLTASIFHLCCISLDYY 120
 DB 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDLVLTASIFHLCCISLDYY 120
 QY 121 AICCPOLVYRNKMTPLRIALMLGCGWVPTFISFLPIMOQWNNIGIIDLERSLNQGLQD 180
 DB 121 AICCPOLVYRNKMTPLRIALMLGCGWVPTFISFLPIMOQWNNIGIIDLERSLNQGLQD 180

181 FFAIEKKKFNQNSNSTYCVFMWKPVAITCSVAFYIPFLMLVAYRIYVYVTAKEHAHQI 240
 170 ---IEKRFKNQNSNSTYCVFMWKPVAITCSVAFYIPFLMLVAYRIYVYVTAKEHAHQI 226
 241 OMLQAGASSERPOSADQHSRTHRTETKAATKLCIINGCFCLCWAPFFVTVIVDPFID 300
 227 OMLQAGASSERPOSADQHSRTHRTETKAATKLCIINGCFCLCWAPFFVTVIVDPFID 286
 301 YTVPGQVWTAFLWGLYINSGLNPLFLYAFLNKSPERRAFLLIILCCDDERYRRPSILGQTVPC 360
 287 YTVPGQVWTAFLWGLYINSGLNPLFLYAFLNKSPERRAFLLIILCCDDERYRRPSILGQTVPC 346
 361 STTTINGSTHVLDRDAVECGQWESQCHPPATSPPLVAAQPSDT 402
 347 STTTINGSTHVLDRDAVECGQWESQCHPPATSPPLVAAQPSDT 388

RESULT 10
 AAO19905
 D AAO19905 standard; protein; 388 AA.
 X
 C AAO19905;
 T 11-AUG-2003 (first entry)
 E Human TA4 receptor associated protein swissnew/070528/SH4_CAVPO.
 W Human; G-protein coupled receptor; TA4 receptor; receptor; cytosolic;
 W haemostatic; antiaesthetic; cardiant; antidiabetic; anorectic; asthma;
 W neuroprotective; haematological disorder; COPD; cardiovascular disease;
 W CNS disorder; diabetes; obesity; cancer; genito-urinary disorder.
 S Homo sapiens.
 X
 N WC02002101043-A2.
 D 19-DEC-2002.
 X
 F 06-JUN-2002; 2002MO-EP006204.
 R 08-JUN-2001; 2001US-0296447P.
 R 15-NOV-2001; 2001US-0331393P.
 R 17-APR-2002; 2002US-0372811P.
 X
 A (PARB) BAYER AG.
 X
 I Zhu Z;
 R WPI; 2003-148806/14.
 T Novel polynucleotide encoding G-protein coupled receptor, TA4 receptor,
 T useful for treating hematological disorders, asthma, cardiovascular
 T disorders, diabetes, obesity, cancer and genito-urinary disorders.
 S Disclosure; Fig 5; 144pp; English.
 X
 C The present invention provides the protein and coding sequences of human
 C TA4 receptor, which is a G-protein coupled receptor. The sequences are
 C useful in the treatment of hematological disorders, chronic obstructive
 C pulmonary disease, asthma, cardiovascular disorders, central nervous
 C system (CNS) disorders, diabetes, obesity, cancer and genito-urinary
 C disorders. The present sequence is the protein swissnew/070528/SH4_CAVPO
 X Sequence 388 AA;
 Q
 Query Match 91.6%; Score 1954; DB 6; Length 388;
 Best Local Similarity 92.0%; Pred. No. 1.2e-204;
 Matches 370; Conservative 8; Mismatches 10; Indels 14; Gaps 1;
 Y 1 MDKLDANVSSEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNYFIV 60
 b 1 MDKLDANVSSEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNYFIV 60

QY 61 SLAFADLLSVLMPFGALIELVQDIWYGEVFCVLTSLDVLTTASIFHLCCISLDYV 120
 DB 61 SLAFADLLSVLMPFGALIELVQDIWYGEVFCVLTSLDVLTTASIFHLCCISLDYV 120
 QY 121 AICCPQLVYRNKMTPLRIALMLGGCWVITPFIISFUPIMQWNNIGIIDLERSLNQGLQD 180
 DB 121 AICCPQLVYRNKMTPLRIALMLGGCWVITPFIISFUPIMQWNNIGIIDLERSLNQGLQD 169
 QY 181 FFAIEKKKFNQNSNSTYCVFMWKPVAITCSVAFYIPFLMLVAYRIYVYVTAKEHAHQI 240
 DB 170 ---IEKRFKNQNSNSTYCVFMWKPVAITCSVAFYIPFLMLVAYRIYVYVTAKEHAHQI 226
 QY 241 OMLQAGASSERPOSADQHSRTHRTETKAATKLCIINGCFCLCWAPFFVTVIVDPFID 300
 DB 227 OMLQAGASSERPOSADQHSRTHRTETKAATKLCIINGCFCLCWAPFFVTVIVDPFID 286
 QY 301 YTVPGQVWTAFLWGLYINSGLNPLFLYAFLNKSPERRAFLLIILCCDDERYRRPSILGQTVPC 360
 DB 287 YTVPGQVWTAFLWGLYINSGLNPLFLYAFLNKSPERRAFLLIILCCDDERYRRPSILGQTVPC 346
 QY 361 STTTINGSTHVLDRDAVECGQWESQCHPPATSPPLVAAQPSDT 402
 DB 347 STTTINGSTHVLDRDAVECGQWESQCHPPATSPPLVAAQPSDT 388

RESULT 11
 AAR57030
 ID AAR57030 standard; protein; 406 AA.
 XX
 AC AAR57030;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAR-1995 (first entry)
 XX
 DE Rat 5-HT4 receptor encoded by S10-95 cDNA clone.
 XX
 KW 5-HT4 serotonin receptor; 5-HT4R; 5-HT4A; adenylyate cyclase; agonist.
 XX
 OS Rattus rattus.
 XX
 PN WO9414957-A2.
 XX
 PD 07-JUL-1994.
 XX
 PF 22-DEC-1993; 93WO-US012586.
 XX
 PR 24-DEC-1992; 92US-00996772.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Gerald C, Hartig P, Branchek TA, Weinschank RL;
 XX
 DR WPI; 1994-234695/28.
 XX
 DR N-PSDB; AAQ57030.
 XX
 PT Mammalian 5-HT4 serotonin receptor, corresp. DNA, probes, anti-sense
 PT oligonucleotide(s) and antibodies - useful for treating conditions
 PT involving abnormal 5-HT4 receptor expression, for screening for
 PT (ant)agonists, prodn. of transgenic animals etc.
 XX
 PS Disclosure; Page 88-91; 161pp; English.
 XX
 CC An isolated DNA molecule encoding a mammalian 5-HT4 receptor is claimed,
 CC having the sequence H2N-V-X-COOH wherein V is bp 101-1177 of AAQ68828 and
 CC X is bps 1178-1261 of AAQ68828 or X is bps 1127-1267 of AAQ68829. S10 is
 CC a 270 bp fragment identified when rat brain cDNA was used as template in
 CC a PCR with the degenerate primers 3.17 (AAQ68832) and 5.5 (AAQ68833)
 CC derived from well conserved regions among several serotonin receptors in
 CC the 3rd and 5th putative transmembrane domains. The peptide sequence
 CC corresp. to the S10 PCR clone contd. a transmembrane IV-like domain and
 CC the clone represents a potentially new serotonin receptor. By direct PCR
 CC analysis of bacterial pools, sib selection and filter hybridisation, two

CC full-length cDNA clones (S10-87, 5.5kb; and S10-95, 4.5kb) were
CC determined. The peptide sequences are only 96.7% identical diverging in
CC the second half of the C-terminal tails, downstream of posn. 359. The
CC entire 3' untranslated regions are totally divergent. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX
SO
Sequence 406 AA:

Query Match 88.1%; Score 1879; DB 2; Length 406;
Best Local Similarity 89.0%; Pred. No. 2.1e-196;
Matches 355; Conservative 13; Mismatches 17; Indels 14; Gaps 1;

QY	1	MDKLDANVSSBEGFSGSEKVVLLTFSTVILMAILGNLLVMVAVCHDRQLRKIKTNYIFV	60
Db	1	MDRLDANVSSNEGFGSEKVVLLTFANVILMAILGNLLVMVAVCHDRQLRKIKTNYIFV	60
QY	61	SLAFADLLAVSLVMPFGAIEALVQDIWIYGVFCLVRTSLDVLTTTASIIFHLCCISLDRY	120
Db	61	SLAFADLLVSLVNAFGAIEALVQDIWIFGEMFCLVRTSLDVLTTTASIIFHLCCISLDRY	120
QY	121	AICCOPLVVRNKMTPRLIALMGGCWIPITFISFLPIMOGMNNIGIDILERSINOGLOQD	180
Db	121	AICCOPLVVRNKMTPRLIALMGGCWIPWFI SFLPIMOGMNNIGIVDV-----	169
QY	181	FHAIEKRKFNQNSNTYCVFMVNPYAITCSVAFYIPFLLMVLAYRYIVYTAKEHAQOI	240
Db	170	---IEKRKFHNNSNTPCFVMVNPYAITCSVAFYIPFLLMVLAYRYIVYTAKEHAQOI	226
QY	241	QMLORAGASSRSRQSDOHSHTHRMRTETKAATLCTIIMGCFCGLCWAPFVTNIVDPPID	300
Db	227	HMLORAGATSSRPQADHSHTHRMRTETKAATLCLVIMGCFCCWAPFVTNIVDPPID	286
QY	301	YTVPGQVWTAFLWLGYNISGLNPFLYAFLNKSFERRAPLIILCCODDERYRPPSILGQTVPC	360
Db	287	YTVPEKVWTAFLWLGYNISGLNPFLYAFLNKSFERRAPLIILCCODDERYRPPILGQTVPC	346
QY	361	STTTINGSTHVLRDVECGQWESCHPPATSPILVAAQP	399
Db	347	STTTINGSTHVLRDVECGQWESRCHLTATSPILVAAQP	385

RESULT 12
AAY14522
ID AAY14522 standard; protein: 360 AA.

AC AAY14522;

XX
DT 31-AUG-1999 (first entry)XX
DE Human serotonin receptor splice variant 5-HT-4(d).

Human; serotonin receptor; splice variant; alternative splicing; 5-HT4;
 KW screening; ligand; central nervous system; CNS; disorder; expression;
 XX gastrointestinal disorder.
 KW

XX Homo sapiens.

XX PN ER2771741-A1.

04-JUN-1999

XX
PF 28-NOV-1997; 97FR-00015037.

XX
PR 28-NOV-1997: 97ER-00015037.XX
XX
PA (INRM } INSERM INST NAT SANTE & RECH MEDICALE.

XX
PI Fischmeister R. Langlois M. Dahmoune Y. Gastineau M. Blondel O;

PI FISCHELS
PI Hoebeke J;

DR WPI; 1999-349539/30.

DR N-PSDB; AAX79307.

XX

PT Splice variants of human 5-HT4 receptor - and corresponding DNA, vectors,
PT antibodies, etc.

Claim 1; Page 44-45; 58pp; French.

This sequence represents the amino acid sequence for the human serotonin receptor splice variant 5-HT4(d). 5-HT4(d) and 5-HT4(c) (AA14521) receptor polypeptides can be used to screen for substances, especially ligands, useful in the treatment of CNS disorders associated with abnormal 5-HT4(c) receptor expression or gastrointestinal disorders associated with abnormal 5-HT4(d) receptor expression.

Sequence 360 AA:

Query Match 88.0%; Score 1878; DB 2; Length 360;
Best Local Similarity 96.2%; Pred. No. 2.3e-196;
Matches 359; Conservative 0; Mismatches 0; Indels 1

Qy	1	MDKLDANVSSSEEGFSGSEVKVLLTFLSTVIMAILGNLLVMVAVCHDRQLRKIKTNFYIV	50
Db	1	MDKLDANVSSSEEGFSGSEVKVLLTFLSTVIMAILGNLLVMVAVCHDRQLRKIKTNFYIV	60
Qy	61	SLAFADLLVSLVMPFGAIBLVODIWIYGEVFCVLVRTSLDVLTTTASIFHLCCISLDRY	120
Db	61	SLAFADLLVSLVMPFGAIBLVODIWIYGEVFCVLVRTSLDVLTTTASIFHLCCISLDRY	120
Qy	121	AICCOPLVYRNKMTPLRIALMLGCGWIPTFISFLPTMOGWNNGIIDLERSINQGLQD	180
Db	121	AICCOPLVYRNKMTPLRIALMLGCGWIPTFISFLPTMOGWNNGIIDL	169
Qy	181	FHAIEKRKFQNSNTCYCFVWVKNPYAITCSVVAFYIPFLLMVLYAYRIYVTAKEHAHQI	240
Db	170	---IEKRKFQNSNTCYCFVWVKNPYAITCSVVAFYIPFLLMVLYAYRIYVTAKEHAHQI	226
Qy	241	QMLQAGASSSRPOSADQSHSTHMRPETAKAATLCILMGCFCLCWAPFVTVINVDPFID	300
Db	227	QMLQAGASSSRPOSADQSHSTHMRPETAKAATLCILMGCFCLCWAPFVTVINVDPFID	286
Qy	301	YTVPCQVWTAFLMWLYGINSGLNPFLYAFLNKSPERRAPFLIILCDDDERRPSILGTQVPC	360
Db	287	YTVPCQVWTAFLMWLYGINSGLNPFLYAFLNKSPERRAPFLIILCDDDERRPSILGTQVPC	346
Qy	361	STTTINGSTHVLR	373
Db	347	STTTINGSTHVLR	359

RESULT 13

RESOL 13
AAY14521
ID AAY14521 standard: protein: 380 AA.

XX AC AAY14521:

31-AUG-1999 (first entry)

XX
DE Human serotonin receptor splice variant 5-HT-4(c).

Human; serotonin receptor; splice variant; alternative splicing; 5-HT4; screening; ligand; central nervous system; CNS; disorder; expression; gastrointestinal disorder.

XX
05
Homo sapiens.

XX PN FR2771741-A1

XX
04-777N-1999
PQ

XX DE 28-NOV-1997. 97FB-00015037

XX 39-NOV-1997. 97FB-00015037

XX
DA (INDM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA

I Fischmeister R, Langlois M, Dahmoune Y, Gastineau M, Blondel O;
 J Hoebeke J;

NR WPI; 1999-349539/30.
 RR N-PSDB; AAX79306.

X Splice variants of human 5-HT4 receptor - and corresponding DNA, vectors,
 T antibodies, etc.

US Claim 1; Page 41-42; 58pp; French.

X This sequence represents the amino acid sequence for the human serotonin
 C receptor splice variant 5-HT4(C). 5-HT4(C) and 5-HT4(d) (AAY14522)
 C receptor polypeptides can be used to screen for substances, especially
 C ligands, useful in the treatment of CNS disorders associated with
 C abnormal 5-HT4(c) receptor expression or gastrointestinal disorders
 C associated with abnormal 5-HT4(d) receptor expression

X Q Sequence 380 AA;

Query Match 88.0%; Score 1877; DB 2; Length 380;
 Best Local Similarity 95.2%; Pred. No. 3.2e-196;
 Matches 359; Conservative 0; Mismatches 4; Indels 14; Gaps 1;

Y 1 MDKLDANVSSEEGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLRLKIKTNVFI 60
 b 1 MDKLDANVSSEEGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLRLKIKTNVFI 60
 Y 61 SLAFADLLSVLVMFPGALIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
 b 61 SLAFADLLSVLVMFPGALIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
 Y 121 AICCPVLVYRNKMTPLRIALMLGGCVIPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
 b 121 AICCPVLVYRNKMTPLRIALMLGGCVIPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
 Y 181 FFAIEKRFKQNSSTYCVFVWVKNKPAITCSVAVFIPELLMVLAYRIYVYVAKHAHQI 240
 b 170 ---IEKRFKQNSSTYCVFVWVKNKPAITCSVAVFIPELLMVLAYRIYVYVAKHAHQI 226
 Y 241 QMLQAGASSESRPQADQHSRTHRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
 b 227 QMLQAGASSESRPQADQHSRTHRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 286
 Y 301 YTVPGQVWTAFLWGLYNSGLNPLFYAFLNKSPRRAPFLIILCCDDERYRRPSILGQTVPC 360
 b 287 YTVPGQVWTAFLWGLYNSGLNPLFYAFLNKSPRRAPFLIILCCDDERYRRPSILGQTVPC 346
 Y 361 STTTINGSTHVLRLDAVE 377
 b 347 STTTINGSTHVLRLDAVE 363

RESULT 14
 BB56322
 D ABB56322 standard; protein; 387 AA.
 C ABB56322;
 X ABB56322;

T 18-FEB-2002 (first entry)

X Non-endogenous human GPCR protein, SEQ ID NO: 437.

X Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 W constitutively activated GPCR; agonist; disease.

X Homo sapiens.
 S Synthetic.

X WO200177172-A2.

X 18-OCT-2001.

PF 05-APR-2001; 2001WO-US011098.
 XX
 PR 07-APR-2000; 2000US-0195747P.
 XX
 PA (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX
 DR WPI; 2001-648759/74.
 DR N-PSDB; AB197958.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.

PS Claim 1; Page 240; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR

XX Sequence 387 AA;

Query Match 87.9%; Score 1874; DB 4; Length 387;
 Best Local Similarity 95.5%; Pred. No. 6.9e-196;
 Matches 359; Conservative 0; Mismatches 3; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEEGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLRLKIKTNVFI 60
 Db 1 MDKLDANVSSEEGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLRLKIKTNVFI 60
 QY 61 SLAFADLLSVLVMFPGALIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
 Db 61 SLAFADLLSVLVMFPGALIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
 QY 121 AICCPVLVYRNKMTPLRIALMLGGCVIPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
 Db 121 AICCPVLVYRNKMTPLRIALMLGGCVIPTFISFLPIMQGNNGIIDLERSLNQGLQD 169
 QY 181 FFAIEKRFKQNSSTYCVFVWVKNKPAITCSVAVFIPELLMVLAYRIYVYVAKHAHQI 240
 Db 170 ---IEKRFKQNSSTYCVFVWVKNKPAITCSVAVFIPELLMVLAYRIYVYVAKHAHQI 226
 QY 241 QMLQAGASSESRPQADQHSRTHRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
 Db 227 QMLQAGASSESRPQADQHSRTHRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 286
 QY 301 YTVPGQVWTAFLWGLYNSGLNPLFYAFLNKSPRRAPFLIILCCDDERYRRPSILGQTVPC 360
 Db 287 YTVPGQVWTAFLWGLYNSGLNPLFYAFLNKSPRRAPFLIILCCDDERYRRPSILGQTVPC 346
 QY 361 STTTINGSTHVLRLDAV 376
 Db 347 STTTINGSTHVLRLTV 362

RESULT 15
 ABB56325
 ID ABB56325 standard; protein; 360 AA.
 XX
 AC ABB56325;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Non-endogenous human GPCR protein, SEQ ID NO: 443.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.

OS Homo sapiens.
XX Synthetic.
PN WO200177172-A2.
XX
XX 18-OCT-2001.
XX
XX 05-APR-2001; 2001WO-US011098.
XX
XX 07-APR-2000; 2000US-0195747P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
XX WPI; 2001-648759/74.
DR N-PSDB; AB197961.
DR
XX
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.
XX
XX Claim 1; Page 244-245; 394pp; English.
XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence is a non-endogenous version of a known human GPCR
XX
SQ Sequence 360 AA;

Query Match 87.8%; Score 1873; DB 4; Length 360;
Best Local Similarity 96.0%; Pred. No. 8e-196;
Matches 358; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNYFIV 60
DB 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNYFIV 60

QY 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
DB 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120

QY 121 AICCPVLYRNKMTPLRIALMLGGCWVPTFISFLPMOGWNNIGIIDLERSLNQGLGOD 180
DB 121 AICCPVLYRNKMTPLRIALMLGGCWVPTFISFLPMOGWNNIGIIDL----- 169

QY 181 FFAIEKKKFNQNSYCVFMNKPVAITCSVVAFTPLLMVLAAYRYVYVTAKEHAHQI 240
DB 170 ---IERKKFNQNSYCVFMNKPVAITCSVVAFTPLLMVLAAYRYVYVTAKEHAHQI 226

QY 241 QMLQKAGASSERPSQADQSTHMRTEKAAKTLCLIMGCFCLCWAPFFVTVNIVDPFID 300
DB 227 QMLQKAGASSERPSQADQSTHMRTEKAAKTLCLIMGCFCLCWAPFFVTVNIVDPFID 286

QY 301 YTVPGQVWTAFLMGLYNSGLNPLFLYAFNLKSFERRAPFLIILCCDDERYRPSILGQTVPC 360
DB 287 YTVPGQVWTAFLMGLYNSGLNPLFLYAFNLKSFERRAPFLIILCCDDERYRPSILGQTVPC 346

QY 361 STTTINGSTHVL 373
DB 347 STTTINGSTHVL 359

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: August 5, 2004, 13:33:24 ; Search time 19 seconds
(without alignments)
1092.297 Million cell updates/sec

itle: US-10-018-257A-2

effect score: 2133
equence: 1 MDKLDANVSSEGGSGVEKV.....ESQCHPATPLVAAOPSDT 402

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

earched: 389414 seqs, 51625971 residues

otal number of hits satisfying chosen parameters: 389414

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pcp:*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pcp:*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pcp:*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pcp:*
- 5: /cgn2_6/prodata/2/iaa/6C COMB.pcp:*
- 6: /cgn2_6/prodata/2/iaa/6D COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result. No.	Score	Match	Length	ID	Description
1	2042	95.7	388	1	US-08-446-822-8
2	2042	95.7	388	4	US-09-328-314-8
3	2042	95.7	388	5	PCT-US93-12586-8
4	1886	88.4	406	4	US-09-328-314-4
5	1884	88.3	406	1	US-07-996-772A-4
6	1884	88.3	406	1	US-08-446-822-4
7	1884	88.3	406	5	PCT-US93-12586-4
8	1878	88.0	360	4	US-09-555-313B-4
9	1877	88.0	360	4	US-09-555-313B-24
10	1877	88.0	760	4	US-09-555-313B-2
11	1769	82.9	387	1	US-07-996-772A-2
12	1769	82.9	387	1	US-08-446-822-2
13	1769	82.9	387	4	US-09-328-314-2
14	1769	82.9	387	5	PCT-US93-12586-2
15	1239	58.1	261	1	US-08-446-822-15
16	1239	58.1	261	4	US-09-328-314-15
17	1239	58.1	261	5	PCT-US93-12586-15
18	939	44.0	178	1	US-07-996-772A-6
19	939	44.0	178	1	US-08-446-822-6
20	939	44.0	178	4	US-09-328-314-6
21	939	44.0	178	5	PCT-US93-12586-6
22	582.5	27.3	446	1	US-07-626-618A-21
23	582.5	27.3	446	1	US-08-333-977-21
24	580.5	27.2	446	2	US-07-969-267B-4
25	580.5	27.2	446	4	US-09-168-510-4
26	569	26.7	483	1	US-08-194-338-7
27	566	26.5	418	3	US-08-817-869-12

28	565.5	26.5	417	5	PCT-US91-00909-2	Sequence 2, Appli
29	563.5	26.4	446	1	US-07-626-618A-22	Sequence 22, Appl
30	563.5	26.4	446	1	US-08-333-977-22	Sequence 22, Appl
31	563.5	26.4	477	2	US-07-969-267B-2	Sequence 2, Appli
32	563.5	26.4	477	4	US-09-168-510-2	Sequence 2, Appli
33	562.5	26.4	475	1	US-07-686-591-4	Sequence 4, Appli
34	562.5	26.4	475	1	US-07-970-715-4	Sequence 4, Appli
35	562.5	26.4	487	1	US-08-444-734A-2	Sequence 2, Appli
36	561.5	26.3	477	1	US-07-791-936A-2	Sequence 2, Appli
37	561.5	26.3	477	1	US-08-383-781B-2	Sequence 2, Appli
38	559	26.2	358	2	US-08-748-485-6	Sequence 6, Appli
39	550	25.8	413	5	PCT-US91-00909-4	Sequence 4, Appli
40	549.5	25.8	413	1	US-08-087-772A-17	Sequence 17, Appl
41	549.5	25.8	417	1	US-08-194-338-8	Sequence 8, Appli
42	549	25.7	365	2	US-08-467-559B-9	Sequence 9, Appli
43	547	25.6	413	1	US-08-444-734A-5	Sequence 5, Appli
44	547	25.6	413	2	US-08-467-568-12	Sequence 12, Appl
45	547	25.6	413	2	US-09-030-582-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-446-822-8
Sequence 9, Application US/08446822
Patent No. 5766879
GENERAL INFORMATION:
APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,822
FILING DATE: June 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-822-8

Query Match	95.7%	Score 2042;	DB 1;	Length 388;
Best Local Similarity	96.5%	Pred. No. 5.7e-156;		
Matches 388;	Conservative	0;	Mismatches	0;
			Indels	14;
			Gaps	1;
QY	1	MDKLDANVSSEGGSGVEKVLLTFLSTVILMAILGNLLVMVAVCDQLRKIKNTYIV	60	
Db	1	MDKLDANVSSEGGSGVEKVLLTFLSTVILMAILGNLLVMVAVCDQLRKIKNTYIV	60	
QY	61	SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVRLTSLDVLTTTASTFHLCCISLDRIY	120	
Db	61	SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVRLTSLDVLTTTASTFHLCCISLDRIY	120	

121 ATCCQPLVYRNKMTPLRIALMLGGCWVITPFIISFLPIMQGNWNIIGIIDLERSINQGLQD 180
 121 ATCCQPLVYRNKMTPLRIALMLGGCWVITPFIISFLPIMQGNWNIIGIIDLERSINQGLQD 169
 181 FNAIEKRFKQNSNSTCYCFMKNKPYAITCSVVAFYIPFLLMVLAYRIYVYTAKEHAQI 240
 170 ---IEKRFKQNSNSTCYCFMKNKPYAITCSVVAFYIPFLLMVLAYRIYVYTAKEHAQI 226
 241 QMLQAGASSESRQSDQHSRMTETKAATLCIIMGCFCCLWAPFFVTNIVDPFID 300
 227 QMLQAGASSESRQSDQHSRMTETKAATLCIIMGCFCCLWAPFFVTNIVDPFID 286
 301 YTPGQVMTAFWLGVNSGLNPFYAFLNKSFRRAPFLIILCCDDERYRPSILGQTVPC 360
 287 YTPGQVMTAFWLGVNSGLNPFYAFLNKSFRRAPFLIILCCDDERYRPSILGQTVPC 346
 361 STTTINGSTHVLDAVECGGQWESQCHPPATSPLVAAQPSDT 402
 347 STTTINGSTHVLDAVECGGQWESQCHPPATSPLVAAQPSDT 388

RESULT 2
 US-09-328-314-8
 ; Sequence 8, Application US/09328314
 ; Patent No. 6331401
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe
 ; APPLICANT: Hartig, Paul R.
 ; APPLICANT: Branchek, Theresa
 ; APPLICANT: Weinshank, Richard L.
 ; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
 ; FILE REFERENCE: 42667-AZ-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/328,314
 ; CURRENT FILING DATE: 1998-04-03
 ; EARLIER FILING DATE: 08/446,822
 ; EARLIER FILING DATE: 1995-07-31
 ; EARLIER APPLICATION NUMBER: PCT/US93/12586
 ; EARLIER FILING DATE: 1993-12-22
 ; EARLIER APPLICATION NUMBER: 07/996,772
 ; EARLIER FILING DATE: 1992-12-24
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 388
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-328-314-8

Query Match 95.7%; Score 2042; DB 4; Length 388;
 Best Local Similarity 96.5%; Pred. No. 5.7e-156;
 Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
 61 SLAFADLLVSLVMPFGAIELVDIWIYGEVFCVLRVTSIDVLLTTASIFHLCCISLDRIY 120
 61 SLAFADLLVSLVMPFGAIELVDIWIYGEVFCVLRVTSIDVLLTTASIFHLCCISLDRIY 120
 121 ATCCQPLVYRNKMTPLRIALMLGGCWVITPFIISFLPIMQGNWNIIGIIDLERSINQGLQD 180
 121 ATCCQPLVYRNKMTPLRIALMLGGCWVITPFIISFLPIMQGNWNIIGIIDLERSINQGLQD 169
 181 FNAIEKRFKQNSNSTCYCFMKNKPYAITCSVVAFYIPFLLMVLAYRIYVYTAKEHAQI 240
 170 ---IEKRFKQNSNSTCYCFMKNKPYAITCSVVAFYIPFLLMVLAYRIYVYTAKEHAQI 226
 241 QMLQAGASSESRQSDQHSRMTETKAATLCIIMGCFCCLWAPFFVTNIVDPFID 300
 227 QMLQAGASSESRQSDQHSRMTETKAATLCIIMGCFCCLWAPFFVTNIVDPFID 286

301 YTPGQVMTAFWLGVNSGLNPFYAFLNKSFRRAPFLIILCCDDERYRPSILGQTVPC 360
 287 YTPGQVMTAFWLGVNSGLNPFYAFLNKSFRRAPFLIILCCDDERYRPSILGQTVPC 346
 361 STTTINGSTHVLDAVECGGQWESQCHPPATSPLVAAQPSDT 402
 347 STTTINGSTHVLDAVECGGQWESQCHPPATSPLVAAQPSDT 388

RESULT 3
 PCT-US93-12586-8
 ; Sequence 8, Application PC/TUS9312586
 ; GENERAL INFORMATION:
 ; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
 ; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
 ; TITLE OF INVENTION: AND USING THEREOF
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM
 ; STREET: 30 ROCKEFELLER PLAZA
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/12586
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, P., John
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 977-9550
 ; TELEFAX: (212) 664-0525
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 388 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US93-12586-8

Query Match 95.7%; Score 2042; DB 5; Length 388;
 Best Local Similarity 96.5%; Pred. No. 5.7e-156;
 Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
 61 SLAFADLLVSLVMPFGAIELVDIWIYGEVFCVLRVTSIDVLLTTASIFHLCCISLDRIY 120
 61 SLAFADLLVSLVMPFGAIELVDIWIYGEVFCVLRVTSIDVLLTTASIFHLCCISLDRIY 120
 121 ATCCQPLVYRNKMTPLRIALMLGGCWVITPFIISFLPIMQGNWNIIGIIDLERSINQGLQD 180
 121 ATCCQPLVYRNKMTPLRIALMLGGCWVITPFIISFLPIMQGNWNIIGIIDLERSINQGLQD 169
 181 FNAIEKRFKQNSNSTCYCFMKNKPYAITCSVVAFYIPFLLMVLAYRIYVYTAKEHAQI 240
 170 ---IEKRFKQNSNSTCYCFMKNKPYAITCSVVAFYIPFLLMVLAYRIYVYTAKEHAQI 226
 241 QMLQAGASSESRQSDQHSRMTETKAATLCIIMGCFCCLWAPFFVTNIVDPFID 300
 227 QMLQAGASSESRQSDQHSRMTETKAATLCIIMGCFCCLWAPFFVTNIVDPFID 286
 301 YTPGQVMTAFWLGVNSGLNPFYAFLNKSFRRAPFLIILCCDDERYRPSILGQTVPC 360

b 287 YTVPGQVMTAFVLWGLYNSGLNPFYAFVFNKSFRAFLIILCCDDERYRPSILGQTVPC 346
y 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 402
b 347 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 388

RESULT 4
S-09-328-314-4
Sequence 4, Application US/09328314
Patent No. 6331401
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS AND USES THEREOF
FILE OF INVENTION: 42667-AZ-PCT-US
CURRENT APPLICATION NUMBER: US/09/328,314
EARLIER FILING DATE: 1998-04-03
EARLIER APPLICATION NUMBER: 08/446,822
EARLIER FILING DATE: 1995-07-31
EARLIER APPLICATION NUMBER: PCT/US93/12586
EARLIER FILING DATE: 1993-12-22
EARLIER APPLICATION NUMBER: 07/996,772
EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 406
TYPE: PRT
ORGANISM: Rattus norvegicus
S-09-328-314-4

Query Match 88.4%; Score 1886; DB 4; Length 406;
Best Local Similarity 89.5%; Pred. No. 1.8e-143;
Matches 357; Conservative 12; Mismatches 16; Indels 14; Gaps 1;

y 1 MDKLDANVSSEGGSGVEKVVLLTSTVILMAILGNLLVMVAVCWDRQLRKIKTYPIV 60
b 1 MDKLDANVSSEGGSGVEKVVLLTSTVILMAILGNLLVMVAVCWDRQLRKIKTYPIV 60
y 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
b 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
y 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMOGWNNIGIILDLERSLNOGLGOD 180
b 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMOGWNNIGIILDLERSLNOGLGOD 180
y 181 PHAIEKRKNONSSTYCVFVNKPVAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAQOI 240
b 170 ---IEKRKNHNSSTFCVFNKPYAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAQOI 226
y 241 QMLQAGASSERPSQADQSHRMTETKAATKLCIIMGCFCCLWAPFFVTVNIDPFD 300
b 227 QMLQAGATSSRPQTADQSHRMTETKAATKLCVINGCFWAPFFVTVNIDPFD 286
y 301 YTVPGQVMTAFVLWGLYNSGLNPFYAFVFNKSFRAFLIILCCDDERYRPSILGQTVPC 360
b 287 YTVPEKVTAFVLWGLYNSGLNPFYAFVFNKSFRAFLIILCCDDERYRPSILGQTVPC 346
y 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQ 399
b 347 STTTINGSTHVLDTVECGQWESRCHLTATSPVAAQ 385

RESULT 5
S-07-996-772A-4
Sequence 4, Application US/07996772A
Patent No. 5472866
GENERAL INFORMATION:

APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Branchek, Theresa A.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/996,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-996-772A-4

Query Match 88.3%; Score 1884; DB 1; Length 406;
Best Local Similarity 89.2%; Pred. No. 2.7e-143;
Matches 356; Conservative 13; Mismatches 16; Indels 14; Gaps 1;

Qy 1 MDKLDANVSSEGGSGVEKVVLLTSTVILMAILGNLLVMVAVCWDRQLRKIKTYPIV 60
Db 1 MDKLDANVSSEGGSGVEKVVLLTSTVILMAILGNLLVMVAVCWDRQLRKIKTYPIV 60
Qy 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
Db 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
Qy 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMOGWNNIGIILDLERSLNOGLGOD 180
Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMOGWNNIGIILDLERSLNOGLGOD 180
Qy 181 PHAIEKRKNONSSTYCVFVNKPVAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAQOI 240
Db 170 ---IEKRKNHNSSTFCVFNKPYAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAQOI 226
Qy 241 QMLQAGASSERPSQADQSHRMTETKAATKLCIIMGCFCCLWAPFFVTVNIDPFD 300
Db 227 QMLQAGATSSRPQTADQSHRMTETKAATKLCVINGCFWAPFFVTVNIDPFD 286
Qy 301 YTVPGQVMTAFVLWGLYNSGLNPFYAFVFNKSFRAFLIILCCDDERYRPSILGQTVPC 360
Db 287 YTVPEKVTAFVLWGLYNSGLNPFYAFVFNKSFRAFLIILCCDDERYRPSILGQTVPC 346
Qy 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQ 399
Db 347 STTTINGSTHVLDTVECGQWESRCHLTATSPVAAQ 385

RESULT 6
US-08-446-822-4

; Sequence 4, Application US/08446822
; Patent No. 5766879

; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,822
; FILING DATE: June 1, 1995

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/WAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-822-4

Query Match 88.3%; Score 1884; DB 1; Length 406;
Best Local Similarity 89.2%; Pred. No. 2.7e-143;
Matches 356; Conservative 13; Mismatches 16; Indels 14; Gaps 1;
QY 1 MDKLDANVSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTYFIV 60
DB 1 MDKLDANVSSNEGFGSVEKVVLLTFPAMVILMAILGNLLVMVAVCEDRQLRKIKTYFIV 60
QY 61 SLAFADLLSVLVMPFGAIELVODIMWYGEVFCVLTSLDVLTTASTIHLCCISLDYRY 120
DB 61 SLAFADLLSVLVNAPGAIELVQDIWYFGEVFCVLTSLDVLTTASTIHLCCISLDYRY 120
QY 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNQGLQD 180
DB 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNQGLQD 180
QY 181 FPAIEKRFKNSNSTCYFVMNKPVAITCSVVAFYIPPELLMVLAYRIYVTAKEHAQI 240
DB 170 ---IEKRFKNSNSTCYFVMNKPVAITCSVVAFYIPPELLMVLAYRIYVTAKEHAQI 226
QY 241 QMLQAGASSESRPQSDQHSRMTETKAAKTLICIMGCFCLWAPFFVTNVDPPID 300
DB 227 QMLQAGATSESRPQTADQHSRMTETKAAKTLICVIMGCFCLWAPFFVTNVDPPID 286
QY 301 YTVPGQVWTAFLMWGLYNSGLNPFYAFNLKSFRAFLIILCCDDERYRPSILGQTVPC 360
DB 287 YTVPEKWTAFMLWGLYNSGLNPFYAFNLKSFRAFLIILCCDDERYRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQP 399
DB 347 STTTINGSTHVLRTDVECGQWESRCHLTATSPVAAQP 385

RESULT 7
PCT-US93-12586-4
; Sequence 4, Application PC/TUS9312586

; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-12586-4

Query Match 88.3%; Score 1884; DB 5; Length 406;
Best Local Similarity 89.2%; Pred. No. 2.7e-143;
Matches 356; Conservative 13; Mismatches 16; Indels 14; Gaps 1;
QY 1 MDKLDANVSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTYFIV 60
DB 1 MDKLDANVSSNEGFGSVEKVVLLTFPAMVILMAILGNLLVMVAVCEDRQLRKIKTYFIV 60
QY 61 SLAFADLLSVLVMPFGAIELVODIMWYGEVFCVLTSLDVLTTASTIHLCCISLDYRY 120
DB 61 SLAFADLLSVLVNAPGAIELVQDIWYFGEVFCVLTSLDVLTTASTIHLCCISLDYRY 120
QY 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNQGLQD 180
DB 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNQGLQD 180
QY 181 FPAIEKRFKNSNSTCYFVMNKPVAITCSVVAFYIPPELLMVLAYRIYVTAKEHAQI 240
DB 170 ---IEKRFKNSNSTCYFVMNKPVAITCSVVAFYIPPELLMVLAYRIYVTAKEHAQI 226
QY 241 QMLQAGASSESRPQSDQHSRMTETKAAKTLICIMGCFCLWAPFFVTNVDPPID 300
DB 227 QMLQAGATSESRPQTADQHSRMTETKAAKTLICVIMGCFCLWAPFFVTNVDPPID 286
QY 301 YTVPGQVWTAFLMWGLYNSGLNPFYAFNLKSFRAFLIILCCDDERYRPSILGQTVPC 360
DB 287 YTVPEKWTAFMLWGLYNSGLNPFYAFNLKSFRAFLIILCCDDERYRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQP 399
DB 347 STTTINGSTHVLRTDVECGQWESRCHLTATSPVAAQP 385

RESULT 8
US-09-555-313B-4
; Sequence 4, Application US/09555313B
; Patent No. 6506580

GENERAL INFORMATION:

APPLICANT: FICSHMEISTER, Rudolph et al.
 TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
 FILE REFERENCE: P06762US00/BAS
 CURRENT APPLICATION NUMBER: US/09/555,313B
 PRIOR FILING DATE: 2002-08-13
 PRIOR FILING DATE: 1997-11-28
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-09-555-313B-4

Query Match 88.0%; Score 1878; DB 4; Length 360;
 Best Local Similarity 96.2%; Pred. No. 7.1e-143;
 Matches 359; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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Y 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
D 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Y 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
D 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Y 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFTSFIPIMQGNNGIIDL----- 169
D 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFTSFIPIMQGNNGIIDL----- 169
Y 181 FPAIEKRFNONSSTYCVFVWVNPYAITCSVAFYIPFLMWLAYRYIYVTAKEHAQI 240
D 170 ---IEKRFNONSSTYCVFVWVNPYAITCSVAFYIPFLMWLAYRYIYVTAKEHAQI 226
Y 241 QMLORAGASSESRPOSADQHSRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 300
D 227 QMLORAGASSESRPOSADQHSRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 286
Y 301 YTPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDERYRRPSILGQTPC 360
D 287 YTPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDERYRRPSILGQTPC 346
Y 361 STTTINGSTHVL 373
D 347 STTTINGSTHVL 359

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RESULT 9

S-09-555-313B-24
 Sequence 24, Application US/09555313B
 Patent No. 6506580
 GENERAL INFORMATION:
 APPLICANT: FICSHMEISTER, Rudolph et al.
 TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
 FILE REFERENCE: P06762US00/BAS
 CURRENT APPLICATION NUMBER: US/09/555,313B
 PRIOR FILING DATE: 2002-08-13
 PRIOR FILING DATE: 1997-11-28
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 24
 LENGTH: 380
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-09-555-313B-24

Query Match 88.0%; Score 1877; DB 4; Length 380;
 Best Local Similarity 95.2%; Pred. No. 9e-143;

Matches 359; Conservative 0; Mismatches 4; Indels 14; Gaps 1;

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Qy 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Db 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Qy 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Db 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Qy 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFTSFIPIMQGNNGIIDLERSLNQGLQD 180
Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFTSFIPIMQGNNGIIDL----- 169
Qy 181 FPAIEKRFNONSSTYCVFVWVNPYAITCSVAFYIPFLMWLAYRYIYVTAKEHAQI 240
Db 170 ---IEKRFNONSSTYCVFVWVNPYAITCSVAFYIPFLMWLAYRYIYVTAKEHAQI 226
Qy 241 QMLORAGASSESRPOSADQHSRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 300
Db 227 QMLORAGASSESRPOSADQHSRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 286
Qy 301 YTPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDERYRRPSILGQTPC 360
Db 287 YTPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDERYRRPSILGQTPC 346
Qy 361 STTTINGSTHVLDAVE 377
Db 347 STTTINGSTHVLSSGTE 363

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RESULT 10

US-09-555-313B-2
 Sequence 2, Application US/09555313B
 Patent No. 6506580
 GENERAL INFORMATION:
 APPLICANT: FICSHMEISTER, Rudolph et al.
 TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
 FILE REFERENCE: P06762US00/BAS
 CURRENT APPLICATION NUMBER: US/09/555,313B
 PRIOR FILING DATE: 2002-08-13
 PRIOR FILING DATE: 1997-11-28
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 760
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-555-313B-2

Query Match 88.0%; Score 1877; DB 4; Length 760;
 Best Local Similarity 95.2%; Pred. No. 1.8e-142;
 Matches 359; Conservative 0; Mismatches 4; Indels 14; Gaps 1;

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Qy 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Db 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Qy 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Db 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Qy 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFTSFIPIMQGNNGIIDLERSLNQGLQD 180
Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFTSFIPIMQGNNGIIDL----- 169
Qy 181 FPAIEKRFNONSSTYCVFVWVNPYAITCSVAFYIPFLMWLAYRYIYVTAKEHAQI 240
Db 170 ---IEKRFNONSSTYCVFVWVNPYAITCSVAFYIPFLMWLAYRYIYVTAKEHAQI 226
Qy 241 QMLORAGASSESRPOSADQHSRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 300

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Db 227 QMLQAGASSESRPOSADQHSHTMRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 286
QY 301 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDRYRPSILGQTVPC 360
Db 287 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDRYRPSILGQTVPC 346
QY 361 SITTINGSTHVLDAVE 377
Db 347 SITTINGSTHVLSSGTE 363

RESULT 11
US-07-996-772A-2
; Sequence 2, Application US/07996772A
; Patent No. 5472866
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa A.
; APPLICANT: Weinstank, Richard U.
; TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/996,772A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667/JPW/TBP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-996-772A-2

Query Match 82.9%; Score 1769; DB 1; Length 387;
Best Local Similarity 88.7%; Pred. No. 4.1e-134;
Matches 338; Conservative 11; Mismatches 18; Indels 14; Gaps 1;
QY 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Db 1 MDRLDANVSSEGGSGVEKVVLLTFFAMVILMAILGNLLVMVAVCDRLRKIKNTYFIV 60
QY 61 SLAFADLLSVLMPFGAIELVDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDRIY 120
Db 61 SLAFADLLSVLWNAFGAIELVDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDRIY 120
QY 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNWNIIGIDLSRLNQLGQD 180
Db 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNWNIIGIDV----- 169
QY 181 FHAIKPKFNQNSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLYYRIYVTAKEHAQI 240
Db 181 FHAIKPKFNQNSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLYYRIYVTAKEHAQI 240

Db 170 ---IEKKFNHNSNTFCVFMVKNKPYAITCSVVAFYIPFLMLVLYYRIYVTAKEHAQI 226
QY 241 QMLQAGASSESRPOSADQHSHTMRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 300
Db 227 QMLQAGASSESRPOSADQHSHTMRMTETKAATKLCIIMGCFCLCWAPFFVTNIVDPFID 286
QY 301 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDRYRPSILGQTVPC 360
Db 287 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSFRAFLIILCCDDRYRPSILGQTVPC 346
QY 361 SITTINGSTHVLDAVECGQ 381
Db 347 SITTINGSTHVLRYTVLHSGQ 367

RESULT 12
US-08-446-822-2
; Sequence 2, Application US/08446822
; Patent No. 5766879
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,822
; FILING DATE: June 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-822-2

Query Match 82.9%; Score 1769; DB 1; Length 387;
Best Local Similarity 88.7%; Pred. No. 4.1e-134;
Matches 338; Conservative 11; Mismatches 18; Indels 14; Gaps 1;
QY 1 MDKLDANVSSEGGSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
Db 1 MDRLDANVSSEGGSGVEKVVLLTFFAMVILMAILGNLLVMVAVCDRLRKIKNTYFIV 60
QY 61 SLAFADLLSVLMPFGAIELVDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDRIY 120
Db 61 SLAFADLLSVLWNAFGAIELVDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDRIY 120
QY 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNWNIIGIDLSRLNQLGQD 180
Db 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNWNIIGIDV----- 169
QY 181 FHAIKPKFNQNSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLYYRIYVTAKEHAQI 240
Db 170 ---IEKKFNHNSNTFCVFMVKNKPYAITCSVVAFYIPFLMLVLYYRIYVTAKEHAQI 226

Y 241 OMLORAGASERPOSADQHSRTHRMETETKAATLCIIMGCFCCLWAPFFVTVNDPFD 300
b 227 OMLORAGATSESPQADQHSRTHRMETETKAATLCVIMGCFCFWAPFFVTVNDPFD 286
Y 301 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSPRRAFLLILCCDDRYRRPSPILGQTVPC 360
b 287 YTVPEKWTAFWGLYNSGLNPFYAFLNKSPRRAFLLILCCDDRYRRPSPILGQTVPC 346
Y 361 STTTINGSTHVLDRDAVECGQ 381
b 347 STTTINGSTHVLRYTVLHSGQ 367

RESULT 13
S-09-328-314-2
Sequence 2, Application US/09328314
Patent No. 6331401
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
FILE REFERENCE: 42667-A2-PCT-US
CURRENT APPLICATION NUMBER: US/09/328,314
CURRENT FILING DATE: 1998-04-03
EARLIER APPLICATION NUMBER: 08/446,822
EARLIER FILING DATE: 1995-07-31
EARLIER APPLICATION NUMBER: PCT/US93/12586
EARLIER FILING DATE: 1993-12-22
EARLIER APPLICATION NUMBER: 07/996,772
EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 387
TYPE: PRT
ORGANISM: Rattus norvegicus
S-09-328-314-2

Query Match 82.9%; Score 1769; DB 4; Length 387;
Best Local Similarity 88.7%; Pred. No. 4.1e-134;
Matches 338; Conservative 11; Mismatches 18; Indels 14; Gaps 1;
Y 1 MDKLDANVSSEBGFSGVEKVVLLTFSTVILMAILGNLLVMVAVCDRLRKIKTYFIV 60
b 1 MDRLDANVSSEBGFSGVEKVVLLTFPAMVILMAILGNLLVMVAVCDRLRKIKTYFIV 60
Y 61 SLAFADLLSVLWMPGALVQDIWYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
b 61 SLAFADLLSVLWNAFAGALVQDIWYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Y 121 AICCPVLVRNKMTPRLIALMLGGCWVPTFISFLPMQGNNGIIDLERSLNOGLQD 180
b 121 AICCPVLVRNKMTPRLIALMLGGCWVPTFISFLPMQGNNGIIDLERSLNOGLQD 169
Y 181 FPAIEKRNQNSSTYCVFMNKPVAITCSVAVYIPFLMLVAYRYVYVTAKEHAQI 240
b 170 ---IERKFNHNSSTFCVFMNKPVAITCSVAVYIPFLMLVAYRYVYVTAKEHAQI 226
Y 241 OMLORAGASERPOSADQHSRTHRMETETKAATLCIIMGCFCCLWAPFFVTVNDPFD 300
b 227 OMLORAGATSESPQADQHSRTHRMETETKAATLCVIMGCFCFWAPFFVTVNDPFD 286
Y 301 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSPRRAFLLILCCDDRYRRPSPILGQTVPC 360
b 287 YTVPEKWTAFWGLYNSGLNPFYAFLNKSPRRAFLLILCCDDRYRRPSPILGQTVPC 346
Y 361 STTTINGSTHVLDRDAVECGQ 381
b 347 STTTINGSTHVLRYTVLHSGQ 367

RESULT 14
PCT-US93-12586-2
Sequence 2, Application PC/TUS9312586
GENERAL INFORMATION:
APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12586
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, P. John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12586-2

Query Match 82.9%; Score 1769; DB 5; Length 387;
Best Local Similarity 88.7%; Pred. No. 4.1e-134;
Matches 338; Conservative 11; Mismatches 18; Indels 14; Gaps 1;
QY 1 MDKLDANVSSEBGFSGVEKVVLLTFSTVILMAILGNLLVMVAVCDRLRKIKTYFIV 60
Db 1 MDRLDANVSSEBGFSGVEKVVLLTFPAMVILMAILGNLLVMVAVCDRLRKIKTYFIV 60
QY 61 SLAFADLLSVLWMPGALVQDIWYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
Db 61 SLAFADLLSVLWNAFAGALVQDIWYGEVFCVLTSLDVLTTASIFHLCCISLDYY 120
QY 121 AICCPVLVRNKMTPRLIALMLGGCWVPTFISFLPMQGNNGIIDLERSLNOGLQD 180
Db 121 AICCPVLVRNKMTPRLIALMLGGCWVPTFISFLPMQGNNGIIDLERSLNOGLQD 169
QY 181 FPAIEKRNQNSSTYCVFMNKPVAITCSVAVYIPFLMLVAYRYVYVTAKEHAQI 240
Db 170 ---IERKFNHNSSTFCVFMNKPVAITCSVAVYIPFLMLVAYRYVYVTAKEHAQI 226
QY 241 OMLORAGASERPOSADQHSRTHRMETETKAATLCIIMGCFCCLWAPFFVTVNDPFD 300
Db 227 OMLORAGATSESPQADQHSRTHRMETETKAATLCVIMGCFCFWAPFFVTVNDPFD 286
QY 301 YTVPGQVWTAFLWGLYNSGLNPFYAFLNKSPRRAFLLILCCDDRYRRPSPILGQTVPC 360
Db 287 YTVPEKWTAFWGLYNSGLNPFYAFLNKSPRRAFLLILCCDDRYRRPSPILGQTVPC 346
QY 361 STTTINGSTHVLDRDAVECGQ 381
Db 347 STTTINGSTHVLRYTVLHSGQ 367

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4 protein - protein search, using sw model

an on: August 5, 2004, 13:35:20 ; Search time 46.Seconds
(without alignments)

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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2042	95.7	388	14	US-10-225-567A-18
5	2037	95.5	388	11	US-09-826-509-439
6	1954	91.6	388	12	US-10-092-771-3
7	1886	88.4	406	9	US-09-989-861-4
8	1879	88.1	387	14	US-10-318-661-23
9	1874	87.9	387	11	US-09-826-509-436
10	1873	87.8	360	11	US-09-826-509-443
11	1872	87.8	380	11	US-09-826-509-441
12	1869.5	87.6	378	11	US-09-826-509-445
13	1769	82.9	387	9	US-09-989-861-2
14	1239	58.1	261	9	US-09-989-861-15
15	939	44.0	178	9	US-09-989-861-6

16	517	28.9	450	14	US-10-299-642-26	Sequence 26, Appl
17	598.5	28.1	508	14	US-10-270-333-69	Sequence 59, Appl
18	591	27.7	445	12	US-10-092-771-7	Sequence 7, Appl
19	587	27.5	446	14	US-10-299-642-30	Sequence 30, Appl
20	582.5	27.3	446	11	US-09-826-509-487	Sequence 487, App
21	582.5	27.3	446	14	US-10-325-567A-98	Sequence 98, Appl
22	582.5	27.3	446	14	US-10-299-642-2	Sequence 2, Appl
23	582.5	27.3	446	14	US-10-299-642-4	Sequence 4, Appl
24	582.5	27.3	446	14	US-10-299-642-6	Sequence 6, Appl
25	582.5	27.3	446	15	US-10-292-798-628	Sequence 628, App
26	581.5	27.3	446	14	US-10-299-642-32	Sequence 32, Appl
27	581	27.2	446	14	US-10-299-642-28	Sequence 28, Appl
28	580.5	27.2	446	14	US-10-277-078-4	Sequence 4, Appl
29	579.5	27.2	446	14	US-10-299-642-16	Sequence 16, Appl
30	577	27.1	382	9	US-09-993-844-5	Sequence 5, Appl
31	577	27.1	382	12	US-10-633-438-62	Sequence 62, Appl
32	568	26.6	463	12	US-10-092-771-5	Sequence 5, Appl
33	567.5	26.6	446	12	US-10-205-331-4	Sequence 20, Appl
34	567.5	26.6	446	14	US-10-299-642-20	Sequence 40, Appl
35	564	26.4	458	12	US-09-964-956-51	Sequence 51, Appl
36	563.5	26.4	477	11	US-09-826-509-493	Sequence 493, App
37	563.5	26.4	477	12	US-09-964-956-47	Sequence 47, Appl
38	563.5	26.4	477	14	US-10-277-078-2	Sequence 2, Appl
39	563.5	26.4	477	14	US-10-225-567A-100	Sequence 100, App
40	563.5	26.4	477	14	US-10-299-642-8	Sequence 8, Appl
41	563.5	26.4	477	14	US-10-299-642-10	Sequence 10, Appl
42	563.5	26.4	477	15	US-10-352-884A-4	Sequence 4, Appl
43	562.5	26.4	446	14	US-10-299-642-22	Sequence 22, Appl
44	562.5	26.4	475	12	US-09-964-956-48	Sequence 48, Appl
45	562.5	26.4	475	14	US-10-299-642-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-989-861-8

```

; Sequence 8, Application US/09989861
; Patent No. US20020081661A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinschenk, Richard L.
; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses
; FILE OF INVENTION: Theosof
; FILE REFERENCE: 42667-AZ-ECT-US
; CURRENT APPLICATION NUMBER: US/09/989,861
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US93/12586
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 07/996,772
; PRIOR FILING DATE: EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-861-8

```

Query Match 95.7%; Score 2042; DB 9; Length 388;

Best Local Similarity 96.5%; Pred. No. 6.6e-185;

Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEGGFSGVEKVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYFV 60

Db 1 MDKLDANVSSEGGFSGVEKVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYFV 60

QY 61 SLAFADLLVSLVMPFGALVELVQDIWIYGEVFLVRTSLDVLTTTASIFHLCCISLDTRY 120

Db 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLRVTSLDVLTASIFHLCCISLDYY 120
Qy 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Db 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Db 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Qy 181 FHAIKRFKFNQNSSTYCVFMNKPVAITCSVAFYIPFLMLVLAIRYIYVTAKEHAHQI 240
Db 170 ---IEKRFKFNQNSSTYCVFMNKPVAITCSVAFYIPFLMLVLAIRYIYVTAKEHAHQI 226
Qy 241 QMLORAGASSESRPQSDQHSRTHMRTETKAATLCIIMGCFCCLWAPFVTVNVDPPFD 300
Db 227 QMLORAGASSESRPQSDQHSRTHMRTETKAATLCIIMGCFCCLWAPFVTVNVDPPFD 286
Qy 301 YTVPGQVMTAFWLGLYNSGLNPLFYAFNLKSFRAFLIILCCDDERYRRPSILGQTVPC 360
Db 287 YTVPGQVMTAFWLGLYNSGLNPLFYAFNLKSFRAFLIILCCDDERYRRPSILGQTVPC 346
Qy 361 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 402
Db 347 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 388

RESULT 2

US-10-157-031-123
; Sequence 123, Application US/10157031
; Publication No. US2003010890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 123
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-123

Query Match 95.7%; Score 2042; DB 14; Length 388;
Best Local Similarity 96.5%; Pred. No. 6.6e-185;
Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
Qy 1 MDKLDANVSSEEGFGSVKVVLLTFLSTVILMAILGNLLVMVAVCMWRQLRKIKTNFYIV 60
Db 1 MDKLDANVSSEEGFGSVKVVLLTFLSTVILMAILGNLLVMVAVCMWRQLRKIKTNFYIV 60
Qy 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLRVTSLDVLTASIFHLCCISLDYY 120
Db 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLRVTSLDVLTASIFHLCCISLDYY 120
Qy 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Db 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Qy 181 FHAIKRFKFNQNSSTYCVFMNKPVAITCSVAFYIPFLMLVLAIRYIYVTAKEHAHQI 240
Db 170 ---IEKRFKFNQNSSTYCVFMNKPVAITCSVAFYIPFLMLVLAIRYIYVTAKEHAHQI 226
Qy 241 QMLORAGASSESRPQSDQHSRTHMRTETKAATLCIIMGCFCCLWAPFVTVNVDPPFD 300
Db 227 QMLORAGASSESRPQSDQHSRTHMRTETKAATLCIIMGCFCCLWAPFVTVNVDPPFD 286
Qy 301 YTVPGQVMTAFWLGLYNSGLNPLFYAFNLKSFRAFLIILCCDDERYRRPSILGQTVPC 360
Db 287 YTVPGQVMTAFWLGLYNSGLNPLFYAFNLKSFRAFLIILCCDDERYRRPSILGQTVPC 346
Qy 361 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 402
Db 347 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 388

RESULT 4

US-10-225-567A-18
; Sequence 18, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19

Qy 361 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 402
Db 347 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 388
RESULT 3
US-10-157-031-124
; Sequence 124, Application US/10157031
; Publication No. US2003010890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 124
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-124

Query Match 95.7%; Score 2042; DB 14; Length 388;
Best Local Similarity 96.5%; Pred. No. 6.6e-185;
Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
Qy 1 MDKLDANVSSEEGFGSVKVVLLTFLSTVILMAILGNLLVMVAVCMWRQLRKIKTNFYIV 60
Db 1 MDKLDANVSSEEGFGSVKVVLLTFLSTVILMAILGNLLVMVAVCMWRQLRKIKTNFYIV 60
Qy 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLRVTSLDVLTASIFHLCCISLDYY 120
Db 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLRVTSLDVLTASIFHLCCISLDYY 120
Qy 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Db 121 AICCPQLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Qy 181 FHAIKRFKFNQNSSTYCVFMNKPVAITCSVAFYIPFLMLVLAIRYIYVTAKEHAHQI 240
Db 170 ---IEKRFKFNQNSSTYCVFMNKPVAITCSVAFYIPFLMLVLAIRYIYVTAKEHAHQI 226
Qy 241 QMLORAGASSESRPQSDQHSRTHMRTETKAATLCIIMGCFCCLWAPFVTVNVDPPFD 300
Db 227 QMLORAGASSESRPQSDQHSRTHMRTETKAATLCIIMGCFCCLWAPFVTVNVDPPFD 286
Qy 301 YTVPGQVMTAFWLGLYNSGLNPLFYAFNLKSFRAFLIILCCDDERYRRPSILGQTVPC 360
Db 287 YTVPGQVMTAFWLGLYNSGLNPLFYAFNLKSFRAFLIILCCDDERYRRPSILGQTVPC 346
Qy 361 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 402
Db 347 SITTINGSTHVLRAVECGGWESQCHPPATSPPLVAAQPSDT 388

Prior Application Number: 60/257,144

Prior Filing Date: 2000-12-19

Number of Seq ID NOS: 2292

Software: Patent in version 3.1

Seq ID No 18

Length: 388

Type: PRT

Organism: Homo sapiens

3-10-225-567A-18

Query Match 95.7%; Score 2042; DB 14; Length 388;

Best Local Similarity 96.5%; Pred. No. 6.6e-185;

Matches 388; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLKIKNTYFIV 60

1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLKIKNTYFIV 60

61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVARTSLDVLTTASTIFHLCCISLDYY 120

61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVARTSLDVLTTASTIFHLCCISLDYY 120

121 AICCPVLRNKMTPRLRIALMLGGCWIPFTISFLPIMQGNNGIIDLRLSLNQLGQD 180

121 AICCPVLRNKMTPRLRIALMLGGCWIPFTISFLPIMQGNNGIIDLRLSLNQLGQD 180

181 FFAIEKRKFQNSNSTYCVFVWVKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAHQI 240

170 ---IEKRKFQNSNSTYCVFVWVKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAHQI 226

241 QMLQAGASSESRPQSDQSHRMTETKAATKLCIIMGCFCLCWAPFFVTVNIDPFID 300

227 QMLQAGASSESRPQSDQSHRMTETKAATKLCIIMGCFCLCWAPFFVTVNIDPFID 286

301 YTVPGQVWTAFLWGLYINSGLNPFYAFNLSFRRAFLIILCCDDERYRPSILGQTVPC 360

287 YTVPGQVWTAFLWGLYINSGLNPFYAFNLSFRRAFLIILCCDDERYRPSILGQTVPC 346

361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 402

347 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 388

RESULT 5

S-09-826-509-439

Sequence 439, Application US/09826509

Publication No. US20030204073A1

GENERAL INFORMATION:

APPLICANT: Lehmann-Bruinsma, Karin

APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

FILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/09/826,509

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/195,747

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE: Patent in Version 2.1

Seq ID No 439

Length: 388

Type: PRT

Organism: Homo sapiens

S-09-826-509-439

Query Match 95.5%; Score 2037; DB 11; Length 388;

Best Local Similarity 96.3%; Pred. No. 2e-184;

Matches 387; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLKIKNTYFIV 60

Db 1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLKIKNTYFIV 60

Qy 61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVARTSLDVLTTASTIFHLCCISLDYY 120

Db 61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVARTSLDVLTTASTIFHLCCISLDYY 120

Qy 121 AICCPVLRNKMTPRLRIALMLGGCWIPFTISFLPIMQGNNGIIDLRLSLNQLGQD 180

Db 121 AICCPVLRNKMTPRLRIALMLGGCWIPFTISFLPIMQGNNGIIDLRLSLNQLGQD 169

Qy 181 FFAIEKRKFQNSNSTYCVFVWVKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAHQI 240

Db 170 ---IEKRKFQNSNSTYCVFVWVKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAHQI 226

Qy 241 QMLQAGASSESRPQSDQSHRMTETKAATKLCIIMGCFCLCWAPFFVTVNIDPFID 300

Db 227 QMLQAGASSESRPQSDQSHRMTETKAATKLCIIMGCFCLCWAPFFVTVNIDPFID 286

Qy 301 YTVPGQVWTAFLWGLYINSGLNPFYAFNLSFRRAFLIILCCDDERYRPSILGQTVPC 360

Db 287 YTVPGQVWTAFLWGLYINSGLNPFYAFNLSFRRAFLIILCCDDERYRPSILGQTVPC 346

Qy 361 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 402

Db 347 STTTINGSTHVLDAVECGQWESQCHPPATSPVAAQPSDT 388

RESULT 6

US-10-092-771-3

Sequence 3, Application US/10092771

Publication No. US20030064381A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR

FILE REFERENCE: D012BNP

CURRENT APPLICATION NUMBER: US/10/092,771

PRIOR FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/273,963

PRIOR FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US 60/278,927

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patent in version 3.0

Seq ID No 3

Length: 388

Type: PRT

Organism: CAVIA PORCELLUS

US-10-092-771-3

Query Match 91.6%; Score 1954; DB 12; Length 388;

Best Local Similarity 92.0%; Pred. No. 1.4e-176;

Matches 370; Conservative 8; Mismatches 10; Indels 14; Gaps 1;

Qy 1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLKIKNTYFIV 60

Db 1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRLKIKNTYFIV 60

Qy 61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVARTSLDVLTTASTIFHLCCISLDYY 120

Db 61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVARTSLDVLTTASTIFHLCCISLDYY 120

Qy 121 AICCPVLRNKMTPRLRIALMLGGCWIPFTISFLPIMQGNNGIIDLRLSLNQLGQD 180

Db 121 AICCPVLRNKMTPRLRIALMLGGCWIPFTISFLPIMQGNNGIIDLRLSLNQLGQD 169

Qy 181 FFAIEKRKFQNSNSTYCVFVWVKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAHQI 240

Db 170 ---IEKRKFQNSNSTYCVFVWVKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAHQI 226

Qy 241 QMLQAGASSESRPQSDQSHRMTETKAATKLCIIMGCFCLCWAPFFVTVNIDPFID 300

Db 227 QVLQAGAPAGRPQADQHS THRMRTETKAAKTLCTIIMCGFCCLWAPFFVTNIVDPFID 286
QY 301 YTVPGQVMTAFMLGYINSGLNPLFYAFLNKSFRAFLIILCCDDERYRPSILGQTVPC 360
Db 287 YTVPGQVMTAFMLGYINSGLNPLFYAFLNKSFRAFLIILCCDDERYRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQPSDT 402
Db 347 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQPIDT 388

RESULT 7

US-09-989-861-4
; Sequence 4, Application US/09989861
; Patent No. US20020081661A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding 5-HT₄ Serotonin Receptors And Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 42667-A2-PCT-US
; CURRENT APPLICATION NUMBER: US/09/989,861
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US93/12586
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 07/996,772
; PRIOR FILING DATE: EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-989-861-4

Query Match 88.4%; Score 1886; DB 9; Length 406;
Best Local Similarity 89.5%; Pred. No. 4.3e-170;
Matches 357; Conservative 12; Mismatches 16; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
Db 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
QY 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDYY 120
Db 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDYY 120
QY 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNOGLGD 180
Db 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNOGLGD 180
QY 181 FHAIEKRFNONSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAQI 240
Db 170 ---LEKRFNONSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAQI 226
QY 241 QMLORAGASSESRPQADQHS THRMRTETKAAKTLCTIIMCGFCCLWAPFFVTNIVDPFID 300
Db 227 QMLORAGASSESRPQADQHS THRMRTETKAAKTLCTIIMCGFCCLWAPFFVTNIVDPFID 286
QY 301 YTVPGQVMTAFMLGYINSGLNPLFYAFLNKSFRAFLIILCCDDERYRPSILGQTVPC 360
Db 287 YTVPGQVMTAFMLGYINSGLNPLFYAFLNKSFRAFLIILCCDDERYRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQ 399
Db 347 STTTINGSTHVLDAVECGQWESQCHPPATSPLVAAQ 385

RESULT 8

US-10-318-661-23

; Sequence 23, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-23

Query Match 88.1%; Score 1879; DB 14; Length 387;
Best Local Similarity 95.7%; Pred. No. 1.9e-169;
Matches 360; Conservative 0; Mismatches 2; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
Db 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
QY 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDYY 120
Db 61 SLAFADLLVSVLMPFGAIELVQDIWIYGEVCLVRTSLDVLTTASIFHLCCISLDYY 120
QY 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNOGLGD 180
Db 121 AICCPPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIGIIDLERSLNOGLGD 180
QY 181 FHAIEKRFNONSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAQI 240
Db 170 ---LEKRFNONSNTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAQI 226
QY 241 QMLORAGASSESRPQADQHS THRMRTETKAAKTLCTIIMCGFCCLWAPFFVTNIVDPFID 300
Db 227 QMLORAGASSESRPQADQHS THRMRTETKAAKTLCTIIMCGFCCLWAPFFVTNIVDPFID 286
QY 301 YTVPGQVMTAFMLGYINSGLNPLFYAFLNKSFRAFLIILCCDDERYRPSILGQTVPC 360
Db 287 YTVPGQVMTAFMLGYINSGLNPLFYAFLNKSFRAFLIILCCDDERYRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAV 376
Db 347 STTTINGSTHVLRTV 362

RESULT 9

US-09-826-509-436
; Sequence 436, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Kno
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 436
LENGTH: 387
TYPE: PRT
ORGANISM: Homo sapiens
S-09-826-509-436

Query Match 87.9%; Score 1874; DB 11; Length 387;
Best Local Similarity 95.5%; Pred. No. 5.5e-169;
Matches 359; Conservative 0; Mismatches 3; Indels 14; Gaps 1;
Y 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
D 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
Y 61 SLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDYY 120
D 61 SLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDYY 120
Y 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
D 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
Y 181 FHAIKRRKFNQNSSTYCVFMVKNKPYAITCSVAVFYIPFLMVLAYRIYVYVTAKEHAQI 240
D 170 ---LEKRRFNQNSSTYCVFMVKNKPYAITCSVAVFYIPFLMVLAYRIYVYVTAKEHAQI 226
Y 241 QMLQAGASSERPSQADQSHRMTETKAAKTLCTIIMGCFCVLCWAPFFVTNIYVDPFID 300
D 227 QMLQAGASSERPSQADQSHRMTETKAAKTLCTIIMGCFCVLCWAPFFVTNIYVDPFID 286
Y 301 YTVPGQVMTAFIWLGYINSGLNPFLYAFLNKSPRAFLIILCCDDERYRPSILGQTVPC 360
D 287 YTVPGQVMTAFIWLGYINSGLNPFLYAFLNKSPRAFLIILCCDDERYRPSILGQTVPC 346
Y 361 STTTINGSTHVLRYV 376
D 347 STTTINGSTHVLRYV 362

RESULT 10

S-09-826-509-443
Sequence 443, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:

APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 443
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
S-09-826-509-443

Query Match 87.8%; Score 1873; DB 11; Length 360;
Best Local Similarity 96.0%; Pred. No. 6.3e-169;
Matches 358; Conservative 0; Mismatches 1; Indels 14; Gaps 1;
Y 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60

DB 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
QY 61 SLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDYY 120
DB 61 SLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDYY 120
QY 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
DB 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 169
QY 181 FHAIKRRKFNQNSSTYCVFMVKNKPYAITCSVAVFYIPFLMVLAYRIYVYVTAKEHAQI 240
DB 170 ---LEKRRFNQNSSTYCVFMVKNKPYAITCSVAVFYIPFLMVLAYRIYVYVTAKEHAQI 226
QY 241 QMLQAGASSERPSQADQSHRMTETKAAKTLCTIIMGCFCVLCWAPFFVTNIYVDPFID 300
DB 227 QMLQAGASSERPSQADQSHRMTETKAAKTLCTIIMGCFCVLCWAPFFVTNIYVDPFID 286
QY 301 YTVPGQVMTAFIWLGYINSGLNPFLYAFLNKSPRAFLIILCCDDERYRPSILGQTVPC 360
DB 287 YTVPGQVMTAFIWLGYINSGLNPFLYAFLNKSPRAFLIILCCDDERYRPSILGQTVPC 346
QY 361 STTTINGSTHVL 373
DB 347 STTTINGSTHVL 359

RESULT 11

US-09-826-509-441
Sequence 441, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:

APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 441
LENGTH: 380
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-441

Query Match 87.8%; Score 1872; DB 11; Length 380;
Best Local Similarity 95.0%; Pred. No. 8.4e-169;
Matches 358; Conservative 0; Mismatches 5; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
DB 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
QY 61 SLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDYY 120
DB 61 SLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDYY 120
QY 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
DB 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 169
QY 181 FHAIKRRKFNQNSSTYCVFMVKNKPYAITCSVAVFYIPFLMVLAYRIYVYVTAKEHAQI 240
DB 170 ---LEKRRFNQNSSTYCVFMVKNKPYAITCSVAVFYIPFLMVLAYRIYVYVTAKEHAQI 226

QY 241 QMLQAGASSESRPQADQHSRMTETKAAKTLCTIMGCFCLCWAPFFVTNIVDPFID 300
DB 227 QMLQAGASSESRPQADQHSRMTETKAAKTLCTIMGCFCLCWAPFFVTNIVDPFID 286
QY 301 YTVPGQVWTAFLWGLYNSGLNPFYAFNLKSPRAFLIILCCDDRYRRPSILGQTVPC 360
DB 287 YTVPGQVWTAFLWGLYNSGLNPFYAFNLKSPRAFLIILCCDDRYRRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVE 377
DB 347 STTTINGSTHVLSSGTE 363

RESULT 12
US-09-826-509-445
; Sequence 445, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 445
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-445

Query Match 87.6%; Score 1869.5; DB 11; Length 378;
Best Local Similarity 92.8%; Pred. No. 1.4e-168;
Matches 360; Conservative 0; Mismatches 3; Indels 25; Gaps 2;

QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
DB 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
QY 61 SLAFADLLSVLMPFGAIELVDIWIYGEVCLVRLTSLDVLLTTASIFHLCCISLDYY 120
DB 61 SLAFADLLSVLMPFGAIELVDIWIYGEVCLVRLTSLDVLLTTASIFHLCCISLDYY 120
QY 121 AICCPPLVYRNKMTPLRIALMGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
DB 121 AICCPPLVYRNKMTPLRIALMGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 169
QY 181 FHAIEKRFNQNNSSTCYFVMNKPVAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAHQI 240
DB 170 ---IEKRFNQNNSSTCYFVMNKPVAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAHQI 226
QY 241 QMLQAGASSESRPQADQHSRMTETKAAKTLCTIMGCFCLCWAPFFVTNIVDPFID 300
DB 227 QMLQAGASSESRPQADQHSRMTETKAAKTLCTIMGCFCLCWAPFFVTNIVDPFID 286
QY 301 YTVPGQVWTAFLWGLYNSGLNPFYAFNLKSPRAFLIILCCDDRYRRPSILGQTVPC 360
DB 287 YTVPGQVWTAFLWGLYNSGLNPFYAFNLKSPRAFLIILCCDDRYRRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVECGQWESQCHP 388
DB 347 STTTINGSTHVL-----SGCSP 363

RESULT 13
US-09-989-861-2

; Sequence 2, Application US/09989861
; Patent No. US20020081661A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinsbank, Richard L.
; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/989,861
; CURRENT FILING DATE: 2001-11-19
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US93/12586
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 07/996,772
; PRIOR FILING DATE: EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-989-861-2

Query Match 82.9%; Score 1769; DB 9; Length 387;
Best Local Similarity 88.7%; Pred. No. 5e-159;
Matches 338; Conservative 11; Mismatches 18; Indels 14; Gaps 1;
QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
DB 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFIV 60
QY 61 SLAFADLLSVLMPFGAIELVDIWIYGEVCLVRLTSLDVLLTTASIFHLCCISLDYY 120
DB 61 SLAFADLLSVLMPFGAIELVDIWIYGEVCLVRLTSLDVLLTTASIFHLCCISLDYY 120
QY 121 AICCPPLVYRNKMTPLRIALMGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 180
DB 121 AICCPPLVYRNKMTPLRIALMGGCWVPTFISFLPIMQGNNGIIDLERSLNQGLQD 169
QY 181 FHAIEKRFNQNNSSTCYFVMNKPVAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAHQI 240
DB 170 ---IEKRFNQNNSSTCYFVMNKPVAITCSVVAFYIPFLMLVLAIRYIYVTAKEHAHQI 226
QY 241 QMLQAGASSESRPQADQHSRMTETKAAKTLCTIMGCFCLCWAPFFVTNIVDPFID 300
DB 227 QMLQAGASSESRPQADQHSRMTETKAAKTLCTIMGCFCLCWAPFFVTNIVDPFID 286
QY 301 YTVPGQVWTAFLWGLYNSGLNPFYAFNLKSPRAFLIILCCDDRYRRPSILGQTVPC 360
DB 287 YTVPGQVWTAFLWGLYNSGLNPFYAFNLKSPRAFLIILCCDDRYRRPSILGQTVPC 346
QY 361 STTTINGSTHVLDAVECGGQ 381
DB 347 STTTINGSTHVLRLVLSGQ 367

RESULT 14
US-09-989-861-15
; Sequence 15, Application US/09989861
; Patent No. US20020081661A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinsbank, Richard L.
; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/989,861
; CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US93/12586
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 07/996,772
PRIOR FILING DATE: EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
S-09-989-861-15

Query Match 58.1%; Score 1239; DB 9; Length 261;
Best Local Similarity 93.6%; Pred. No. 5.3e-109;
Matches 234; Conservative 0; Mismatches 2; Indels 14; Gaps 1;

Y 127 LVYRNKMTPLRIALMLGGCWVPTFTISFLPIMQGNWNIIGIIDLERSLNQGLGQDFHAIK 186
b 1 LVYRNKMTPLRIALMLGGCWVPTFTISFLPIMQGNWNIIGIIDL-----IEK 46
Y 187 RKFNQNSNSTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAHQIOMLQRA 246
b 47 RKFNQNSNSTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAHQIOMLQRA 106
Y 247 GASSESRRPOSADQHSRMTETKAAKTLCTIIMGCFCLCWAPFFVTNIVDPPIDYTPGQ 306
b 107 GASSESRRPOSADQHSRMTETKAAKTLCTIIMGCFCLCWAPFFVTNIVDPPIDYTPGQ 166
Y 307 VMTAFMLWGLYINSLNPFLYAFINKSFRAFLIILCCDDERYRRPSILGQTPCSTTTIN 366
b 167 VMTAFMLWGLYINSLNPFLYAFINKSFRAFLIILCCDDERYRRPSILGQTPCSTTTIN 226
Y 367 GSTHVLRLDAV 376
b 227 GSTHVLRLYTV 236

RESULT 15
S-09-989-861-6
Sequence 6, Application US/09989861
Patent No. US20020081661A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses
FILE REFERENCE: 42667-AZ-PCT-US
CURRENT APPLICATION NUMBER: US/09/989,861
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US93/12586
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 07/996,772
PRIOR FILING DATE: EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
S-09-989-861-6

Query Match 44.0%; Score 939; DB 9; Length 178;
Best Local Similarity 92.2%; Pred. No. 9.1e-81;
Matches 177; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

Y 127 LVYRNKMTPLRIALMLGGCWVPTFTISFLPIMQGNWNIIGIIDLERSLNQGLGQDFHAIK 186
|||||

Db 1 LVYRNKMTPLRIALMLGGCWVPTFTISFLPIMQGNWNIIGIDL-----IEK 46
QY 187 RKFNQNSNSTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAHQIOMLQRA 246
Db 47 RKFNQNSNSTYCVFMVKNKPYAITCSVVAFYIPFLMLVLAAYRIYVTAKEHAHQIOMLQRA 106
QY 247 GASSESRRPOSADQHSRMTETKAAKTLCTIIMGCFCLCWAPFFVTNIVDPPIDYTPGQ 306
Db 107 GASSESRRPOSADQHSRMTETKAAKTLCTIIMGCFCLCWAPFFVTNIVDPPIDYTPGQ 166
QY 307 VMTAFMLWGLYIN 318
Db 167 VMTAFMLWGLYIN 178

Search completed: August 5, 2004, 13:41:22
Job time : 48 secs

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M protein - protein search, using sw model
un on: August 5, 2004, 13:31:49 ; Search time 17 Seconds
(without alignments)
2274.647 Million cell updates/sec

file: US-10-018-257A-2
effect score: 2133
sequence: 1 MDKLDANVSSBEGFGVEKV.....BSQCHPRATSPVLAQPSDT 402

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

sarched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters: 283366

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase :
1: PIR 78:
2: PIR1:
3: PIR2:
4: PIR3:
5: PIR4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1886	88.4	406	2 S55549	serotonin 4 recept
2	1789	82.9	387	2 S55550	5-HT4S receptor -
3	755	35.4	144	2 S66493	serotonin receptor
4	700	32.8	151	2 S66495	serotonin receptor
5	648	30.4	137	2 S66487	serotonin receptor
6	617	28.9	450	2 A55986	dopamine receptor
7	610	28.6	353	2 I50475	dopamine D1 recept
8	591.5	27.7	459	2 A56849	dopamine receptor-
9	588.5	27.6	451	2 I51659	dopamine D1A recept
10	582.5	27.3	446	1 DYH0D1	dopamine receptor
11	581.5	27.3	446	2 I47217	dopamine receptor
12	580	27.2	465	2 I51661	dopamine D1C recept
13	574	26.9	483	2 A25896	beta-adrenergic re
14	573.5	26.9	386	2 S72168	dopamine receptor
15	568	26.6	463	2 B56849	dopamine receptor-
16	566	26.5	418	1 QRHYB2	beta-2-adrenergic
17	563.5	26.4	477	1 DYH0D5	dopamine receptor
18	562.5	26.4	475	2 A41271	dopamine receptor
19	562.5	26.4	487	1 DYH0D1	dopamine receptor
20	562	26.3	457	2 I51660	dopamine D1B recept
21	559	26.2	358	2 JQ1278	histamine H2 recept
22	556	26.1	415	2 I53040	beta-2 adrenergic
23	554.5	26.0	464	2 S12591	beta-1-adrenergic
24	553.5	25.9	444	2 C55986	dopamine receptor
25	550	25.8	418	2 S00260	beta-2-adrenergic
26	550	25.8	486	2 B55886	dopamine receptor
27	549	25.7	466	2 S36794	beta-1-adrenergic
28	547	25.6	413	1 QRH0B2	beta-2-adrenergic
29	545.5	25.6	359	2 JH0449	histamine H2 recept

30	539.5	25.3	428	2 A55044	beta-4C-adrenergic
31	539	25.3	418	2 S10855	beta-2-adrenergic
32	537.5	25.2	477	1 ORH0B1	beta-1-adrenergic
33	535	25.1	480	2 I53053	beta 1 adrenergic
34	531.5	24.9	359	2 J04120	histamine H2 recept
35	523.5	24.5	385	2 S68780	dopamine D1-like r
36	519.5	24.4	445	2 A48881	serotonin receptor
37	517.5	24.3	420	2 T25689	hypothetical prote
38	516.5	24.2	359	2 A39008	histamine H2 recep
39	516	24.2	476	2 J05042	G protein-coupled
40	514.5	24.1	511	2 S44275	dopamine receptor
41	513	24.1	448	2 A47519	serotonin receptor
42	506	23.7	442	2 S36402	serotonin receptor
43	498.5	23.4	501	2 JH0447	alpha-1A-adrenergi
44	498.5	23.4	572	2 I39369	alpha-1A-adrenergi
45	496.5	23.3	422	2 JH0315	serotonin receptor

ALIGNMENTS

RESULT 1

S55549
serotonin 4 receptor - rat
N:Alternate names: 5-HT receptor 4L
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Nov-1999
C:Accession: S55549; S66494
R:Gerald, C.; Acham, N.; Kao, H.T.; Olsen, M.A.; Laz, T.M.; Schechter, L.E.; Bard, J.A.
R:EMBO J. 14, 2806-2815, 1995
A:Title: The 5-HT(4) receptor: molecular cloning and pharmacological characterization o
A:Reference number: S55549; MUID:95317299; PMID:7796807
A:Accession: S55549
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-406 <GER>
A:Cross-references: GB:U20907; NID:G924640; PIDN:AAC52233.1; PID:G924641
R:Ullmer, C.; Schumk, K.; Kalkman, H.O.; Luebbert, H.
R:FEBS Lett. 370, 215-221, 1995
A:Title: Expression of serotonin receptor mRNAs in blood vessels.
A:Reference number: S66487; MUID:95385798; PMID:7656980
A:Accession: S66494
A:Molecule type: mRNA
A:Residues: 95-259 <ULL>
A:Cross-references: EMBL:Z48153; NID:G984171; PIDN:CAA88170.1; PID:G984172
A:Experimental source: tissue brain
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match	88.4%;	Score 1886;	DB 2;	Length 406;
Best Local Similarity	89.5%;	Pred. No. 6.1e-163;		
Matches 357;	Conservative 12;	Mismatches 16;	Indels 14;	Gaps 1;
QY	1	MDKLDANVSSBEGFGSVEKVLTLFTSTVILMAILGNLLVMVAVCDROLRIKNTYFIV	60	
Db	1	MDRLDANVSSBEGFGSVEKVLTLFTTFAMVILMAILGNLLVMVAVCDROLRIKNTYFIV	60	
QY	61	SLAFADLLVSLVMPFGALVQDIWIYGEVCLVRLTSLDVLTTASIFHLCCISLDYY	120	
Db	61	SLAFADLLVSLVNAFGALVQDIWYGEVCLVRLTSLDVLTTASIFHLCCISLDYY	120	
QY	121	AICCPVLVYRNKNTPLRIALMLGGCWVITPFTISFLPIMOGMNNIGIIDLERSLNOGLQD	180	
Db	121	AICCPVLVYRNKNTPLRIALMLGGCWVITPFWISFLPIMOGMNNIGIVDV	169	
QY	181	PHAIKRFKNQNSSTYCVFMKNPYAITCSVAVYIPFLMLVAYRIYVYAKEHAHQI	240	
Db	170	---IEAKRFHNHNSSTFCVFMKNPYAITCSVAVYIPFLMLVAYRIYVYAKEHAQOI	226	
QY	241	QMLORAGASSSRPOSADQSHRMTETKAAKTLCTIIMGCFCICWAPFFVTNIVDPFD	300	
Db	227	QMLORAGATSSSRPQTADQSHRMTETKAAKTLCTVIMGCFCFCWAPFFVTNIVDPFD	286	


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;Accession: S66487
;Status: preliminary; nucleic acid sequence not shown
;Molecule type: mRNA
;Residues: 1-137 <ULL>
;Cross-references: EMBL:248175; NID:9984242; PIDN:CAA88198.1; PID:9984243
;Superfamily: vertebrate rhodopsin
;Keywords: neurotransmitter receptor

Query Match      30.4%; Score 648; DB 2; Length 137;
Best Local Similarity 80.8%; Pred. No. 2.3e-51;
Matches 122; Conservative 7; Mismatches 8; Indels 14; Gaps 1;

Y 123 CCQPLVYRNKMTPLRLALMLGCGWVPTPISFLPIMQGNNGIIDLERSLNQGLQDPH 182
b 1 CCQPLVYRNKMTPLRLAVALLGCAWPAVLISFLPIMQGNNGITDL----- 47
Y 183 ATEKRFKFNQNSSTYCVFVWVKNPYAITCSVAFYIPFLMLVLYRYIYTAKEHAHQIQM 242
b 48 -TEKRFKFNQNSSTYCVFVWVKNPYAITCSVAFYIPFLMLVLYRYIYTAKEHAHQIQM 106
Y 243 LQKAGASSERPOSADQHSRMRRTETKAAK 273
b 107 LQKAGAPASGRPPSADQHSRMRRTETKAAK 137

RESULT 6
55886
opamine receptor DIA - chicken
;Species: Gallus gallus (chicken)
;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
;Accession: A55886
;Demchynsyn, L.I.; Sugamori, K.S.; Lee, F.J.S.; Hamadanizadeh, S.A.; Niznik, H.B.
; Biol. Chem. 270, 4005-4012, 1995
;Title: The dopamine D1D receptor. Cloning and characterization of three pharmacologica
;Reference number: A55886; MUID:95181368; PMID:7876148
;Accession: A55886
;Status: preliminary; nucleic acid sequence not shown
;Molecule type: DNA
;Residues: 1-450 <DEM>
;Cross-references: GB:I36877
;Note: authors translated the codon MET for residue 427 as Ile, and ACC for residue 440
;Superfamily: vertebrate rhodopsin
;Keywords: neurotransmitter receptor

Query Match      28.9%; Score 617; DB 2; Length 450;
Best Local Similarity 36.4%; Pred. No. 5.3e-48;
Matches 143; Conservative 59; Mismatches 131; Indels 60; Gaps 11;

Y 25 FLSTVILMAILGNLWVAVCHDQRLKIKTNFYVLSLAFADLLSVLWMPGATLVD 84
b 28 FLSTLILTLGNLTVCAAVIRFRLRSKVTNFFVLSLAVSLLVAVLWMPKAVSSIA 87
Y 85 IWTYGEVFCVLTSLDLVLTASIPHLGCSIDRYVAICQQLPVYRNKMTPLRLALMLGG 144
b 88 FWPFGS-FCNIWVAFDIMCSTASILNLCVSDRYWAL-SSPFYERKMTPKAAPMISV 145
Y 145 CWVPTPISFLPIMQGNW--NIGIIDLERSLNQGLQDPHAIKRFKFNQNSSTYCVFM 201
b 146 AWLTSVLISFIPQLNWKHATTSPFLDLNASL-QGISMD-----NCDSS 188
Y 202 VNKPYAITCSVAFYIPFLMLVLYRYIYTAKEHAHQIQMLQRA-----GASS 250
b 189 LNRMYAISLSLISFYIPVAIMIYVTRIYRIAQKQIRRSALERAHVAKNQTSGNRS 248
Y 251 ESRPQSDQHSRMRMTETKAAKTCICMGFCCLWAPFFVTVNIDVPFDIDYTPVGQ---- 306
b 249 SMDCCQPSNFKMSFRRETKVLKTLVINGVFCVWLPFFVLCNMPFCEPTQPSKGAA 308
Y 307 -----VWTAFLWLVINGSLNPFYAFLNKGFRRAPFLIILCDDRRRPSILGQTPVC 360
b 309 FCINSTTFDVFVFWGANGSLNPIIYAF-NADPRKAFSTLLGC-----YRLCPWAGNAL-- 361
Y 361 SITTINGSHTVLRDVCECGQWESQCHPATSP 393
```

```
Db 362 ETVSINN-----GAVFSSQHEPKSSP 384

RESULT 7
150475
dopamine D1 receptor - goldfish
;Species: Carassius auratus (goldfish)
;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
;Accession: I50475
;R;Frail, D.E.; Manselli, A.M.; Witte, D.G.; Lin, C.W.; Steffey, M.E.; Mackenzie, R.G.
; Mol. Pharmacol. 44, 1113-1118, 1993
;Title: Cloning and characterization of a truncated dopamine D1 receptor from goldfish
;Reference number: I50475; MUID:94088471; PMID:8264547
;Accession: I50475
;Status: preliminary; translated from GB/EMBL/DDBJ
;Molecule type: DNA
;Residues: 1-363 <FRA>
;Cross-references: GB:L08602; NID:9212949; PIDN:AAAL6322.1; PID:g212950
;Superfamily: vertebrate rhodopsin
;Keywords: neurotransmitter receptor

Query Match      28.6%; Score 610; DB 2; Length 363;
Best Local Similarity 38.4%; Pred. No. 1.8e-47;
Matches 140; Conservative 65; Mismatches 118; Indels 42; Gaps 11;

QY 1 MDKLDANVSS--BEGFGSVEKVV-LLT--FLSTVILMAILGNLWVAVCWDRQLRKINT 55
Db 1 MAVLDLNLTTVIDSGFMESDRSVRLTGCFLSVLILTLGNLTVCAAVTKFHLRSKVT 60
QY 56 NYFIVSLAFADLLSVLWMPGATLVDQIWIYGEVFCVLTSLDLVLTASIFHLCCIS 115
Db 61 NFFVISTLAVSLLVAVLWMPKAVTEVAGFWPFG-AFCDIIVAFDIMCSTASILNLCVIS 119
QY 116 LDYVVAICQQLPVYRNKMTPLRLALMLGCGWVPTPISFLPIMQGNW--IGIIDLERS 172
Db 120 VDRYWAL-SSPFYERKMTPRVAFWISGATLSVLISFIPVQLKWKHAQPIGFLEVNAS 178
QY 173 LNQSLGQDPHAIKRFKFNQNSSTYCVFVWVKNPYAITCSVAFYIPFLMLVLYRYIYV 232
Db 179 -----RRDLPTDNCDSLNRITYAISLSLISFYIPVAIMIYVYQIVRI 221
QY 233 AKEHAHQIQLORAGASSERPOS-----ADQISHTRM--RTETKAAKTLCIINGCFL 284
Db 222 AQKQIRRSALERAESAQAIRHDSMGSGSNMDLSSPKLSFKRETQVLTSLVINGVFCV 281
QY 285 CWAPFFVTVNIDVPFDIDYTPVG-----QVWTAFLWLVINGSLNPFYAFLNKSFRRAPL 338
Db 282 CMLPFLINCMVFPFCRISNGLPCISPTTFDVFVWFGWANGSLNPIIYAF-NADPRAPA 340
QY 339 IILCC 343
Db 341 ILLGC 345

RESULT 8
A56849
dopamine receptor-like protein D14 - Japanese pufferfish
;Species: Fugu rubripes (Japanese pufferfish)
;Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
;Accession: A56849
;R;Macrae, A.D.; Brenner, S.
; Genomics 25, 436-446, 1995
;Title: Analysis of the dopamine receptor family in the compact genome of the puffer f
;Reference number: A56849; MUID:95309911; PMID:7789977
;Accession: A56849
;Status: preliminary; not compared with conceptual translation
;Molecule type: DNA
;Residues: 1-459 <MAC>
;Cross-references: GB:X80174; NID:g1204089; PIDN:CAA56455.1; PID:g1204090
;Superfamily: vertebrate rhodopsin
;Keywords: neurotransmitter receptor
```

Query Match 27.7%; Score 591.5; DB 2; Length 459;
Best Local Similarity 37.0%; Pred. No. 1.1e-45;
Matches 130; Conservative 60; Mismatches 114; Indels 47; Gaps 9;

QY 16 SVEKVVLLTFLSVILMAILGNLLVMVAVCWDRQLRKIKTNFYVSLA 63
DB 20 SSKRVLTGCLSLIFLTLGNLTVCAVTKFRLSKVTNPFVLSLAISDLVAILNVP 79
QY 76 FGAIELVQDIWIYGEVFLVRLTSLDVLTTASTFHLCCISLDRYAICCCQVLYRNKMT 135
DB 80 WKATKIMGFWPGE-PCNIWAFDLMCTASILNLCVSDRYWAI-SSPFYERKMT 137
QY 136 LRALMLGGCWVPTFISFLPIMQGNWNIIGIDLSRLNGLQGDPHATEKRFKFNONS 195
DB 138 KVACLMSVANTLSLISFIPVQLNW-----HKAQTASYVB-LNG 176
QY 196 TY-----CVMVKNKPAITCSVAFYIPPELLMVLAYRYVTAKEHAHQIOMLORAG 247
DB 177 TYAGDLPPDNCSSLRNTYAISSLSIFVPAIMIVTYTRYIAQKQIRISALERA 236
QY 248 ASSESRPO-----SADQSTHSM--RTETKAATLCILMGCFCLCWAPFFVTNIVDPFI 299
DB 237 ESAQRHSSMGNLSMESCSFMSFKRETKVLTLSVINGVFCVCLWPFILNCWVPC 296
QY 300 DY-----TVPGQVWTAFLWLYGINSGLNPFYAFNLKSFRRAPFLIILCC 343
DB 297 EADDTTDFPCISSTTDPVFWFGWANSNLPIIYAF-NADFRKAFSILLG 346

RESULT 9
151659
dopamine D1A receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51659
R:Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150; PMID:7937989
A:Accession: I51659
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <SUG>
A:Cross-references: EMBL:U07863; NID:G559759; PIDN:AAA50828.1; PID:G559760
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 27.6%; Score 588.5; DB 2; Length 451;
Best Local Similarity 34.5%; Pred. No. 2e-45;
Matches 146; Conservative 64; Mismatches 150; Indels 63; Gaps 13;

QY 16 SVEKVVLLT-----FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYVSLA 63
DB 7 SMDEDVLLTERESSFVLITGCLFSLVILTLGNLTVCAVTRFRLSKVTNPFVSLA 66
QY 64 FADLLVSLVMPGAEIIVQDIWIYGEVFLVRLTSLDVLTTASTFHLCCISLDRYAIC 123
DB 67 VSDLLVAVLMPKVAEIAAGEWPGF-TFCNIWAFDLMCTASILNLCVSDRYWAI- 124
QY 124 CQPLVYRNKMTPLRIALMLGGCWVPTFISFLPIMQGNW--NIGIIDLSRLNGLQGD 180
DB 125 SSPFYERKMTKPAFIMIGVAVTSLVLSFIPVQLNWHKAKTSPFDLNLITLH----- 178
QY 181 FRAIERKFNONSNSYCYFMVKNKPAITCSVAFYIPPELLMVLAYRYVTAKEHAHQI 240
DB 179 -----DRTMDCSSLNRNTYAISSLSIFVPAIMIVTYTRYIAQKQIRI 227
QY 241 QMLQORAGA-----SSESRPOSAD-QHSTHRT-----ETKAATLCIIMGCFCLCWAP 289
DB 228 SALERAHVAKONQNSTNRNSLDCQPPSSLSKTSFKRETKVLTLSVINGVFCVCLWPF 287
QY 290 FVTNIVDPFID-----YTPGQVWTAFLWLYGINSGLNPFYAFNLKSFRRAPFLI 339

Query Match 27.3%; Score 582.5; DB 1; Length 446;
Best Local Similarity 33.7%; Pred. No. 7e-45;
Matches 139; Conservative 67; Mismatches 135; Indels 71; Gaps 12;

QY 7 NVSSEGRGSV-----EKVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYV 60
DB 5 NTSAMDGCLVVERDFSVRLTACFLSLILLSTLLGNLTVCAVTRFRLSKVTNPFVI 64
QY 61 SLAFADLLVSLVMPGAEIIVQDIWIYGEVFLVRLTSLDVLTTASTFHLCCISLDRY 120
DB 65 SLAVSDLLVAVLMPKVAEIAAGEWPGF-TFCNIWAFDLMCTASILNLCVSDRYW 123

Db 288 FILNCIVPFCPSLTSTGTEPFICISSTTDFVFWFGWANSNLPIIYAF-NADFRKAFSN 346
QY 340 ILCCDDERYRPSILGQVPCSTTTTNGSTHVLRA-VECGQWESQCHPPATSPLVAAQ 398
DB 347 LLGC-----YRLCPTSNII--ETVSIINNGAVVSCQEPKGSIPNECNLYLIPHALIC 400
QY 399 PSD 401
DB 401 PED 403

RESULT 10
DYHUDDI
dopamine receptor D1 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: S11377; S11376; S11379
R:Zhou, Q.Y.; Grandy, D.K.; Thambi, L.; Kushner, J.A.; van Tol, H.H.M.; Cone, R.; P.
Nature 347, 76-80, 1990
A:Title: Cloning and expression of human and rat D(1) dopamine receptors.
A:Reference number: S11377; MUID:90370094; PMID:2168520
A:Accession: S11377
A:Molecule type: DNA
A:Residues: 1-446 <ZHO>
A:Cross-references: EMBL:X58987
R:Deary, A.; Gingrich, J.A.; Falardeau, P.; Freneau Jr., R.T.; Bates, M.D.; Caron,
Nature 347, 72-76, 1990
A:Title: Molecular cloning and expression of the gene for a human D(1) dopamine rec
A:Reference number: S11376; MUID:90370093; PMID:2144334
A:Accession: S11376
A:Molecule type: DNA; mRNA
A:Residues: 1-446 <DEA>
A:Cross-references: EMBL:X55760; NID:G30396; PIDN:CAA39286.1; PID:G30397
R:Sunahara, R.K.; Niznik, H.B.; Weiner, D.M.; Stormann, T.M.; Brann, M.R.; Kennedy,
Nature 347, 80-83, 1990
A:Title: Human dopamine D(1) receptor encoded by an intronless gene on chromosome 5
A:Reference number: S11379; MUID:90370095; PMID:1975640
A:Accession: S11379
A:Molecule type: DNA
A:Residues: 1-446 <SUN>
A:Cross-references: GB:X55758; NID:G288931; PIDN:CAA39284.1; PID:G288932
C:Genetics:
A:Gene: GDB:DRD1
A:Cross-references: GDB:125240; OMIM:126449
A:Map position: 5q34-5q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter
P:25-49/Domain: transmembrane #status predicted <TM1>
P:61-87/Domain: transmembrane #status predicted <TM2>
P:98-119/Domain: transmembrane #status predicted <TM3>
P:140-163/Domain: transmembrane #status predicted <TM4>
P:194-214/Domain: transmembrane #status predicted <TM5>
P:215-273/Domain: intracellular #status predicted <CYT>
P:274-295/Domain: transmembrane #status predicted <TM6>
P:313-333/Domain: transmembrane #status predicted <TM7>
P:5-175/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:96-186/Disulfide bonds: #status predicted
P:136-269/Binding site: phosphate (Thr) (covalent) #status predicted
P:259-263/Binding site: phosphate (Ser) (covalent) #status predicted
P:347/Binding site: palmitate (Cys) (covalent) #status predicted

```
Y 121 AICCPQLVTRNKTPLRIALMLGGCWVPTFTFISFLPDMQWNNIGIIDLERSLNQGLQD 180
b 124 AI-SSPFYERKMTKPAAFILISVANTLSVLSPFVQLSWHK-----165
Y 181 FFAIEKRKFQNSNST-----YCFVMNKPVAITCSVVAFFIPPLMLVLAAYRIYVTA 233
b 166 ----AKPTSPSNGNATLAETDNCDSLSRYAISSVISFTPIPAIMIVYTRYRIA 221
Y 234 KEHAHQIQLORAGASSE-----SRPOSADQSHSTRMRTTKAATLCIIM 279
b 222 OKQIRIAALERAHAHAKNCQTTTGGKPFVCSQPESSFKMFKR---ETKVLKTLVIM 278
Y 280 GCEFLCWAFVTVNVDPI-----DYTVGQVWTAFLWGLYNSGLNPFYAFLNKSF 333
b 279 GVFCVCLWFFILNCLPFGSGGETOFFCIDENFTDFVFWFGWANSLSNPITIAF-NADF 337
Y 334 RRAFLIILCDDERYRPSILGTVPCTTTTNG-----STVLRDAV-EC 378
b 338 RKAFTLLGC-----YRLCATNNAITVSNNGAAMFSSHHEPRGSIKEC 385

RESULT 11
opamine receptor - pig
;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
;Accession: I47217
;Grenader, A.C.; O'Rourke, D.A.; Healy, D.P.
m. J. Physiol. 268, F423-F434, 1995
;Title: Cloning of the porcine D1A dopamine receptor gene expressed in renal epithelial
;Reference number: I47217; MUID:95208810; PMID:7900842
;Accession: I47217
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-446 <GRE>
;Cross-references: EMBL:U25681; NID:g808097; PIDN:AAA79848.1; PID:g808098
;Genetics:
;Superfamily: vertebrate rhodopsin
;Keywords: neurotransmitter receptor

Query Match 27.1%; Score 581.5; DB 2; Length 446;
Best Local Similarity 33.9%; Pred. No. 8.6e-45;
Matches 140; Conservative 64; Mismatches 146; Indels 63; Gaps 11;

Y 7 NVSSBEGFQSV-----KVVLTFILSTVILMAILGNLLVMVAVCWDRQLRKIKTYFIV 60
b 5 NTSTMDGTGLVVERDFSRILTACFLSLILSLTLLGLTLCVAVIRFHLRSKVTNFFVI 64
Y 61 SLAFADLLSVLWMPGATLVDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
b 65 SLAVSLLVAVLWMPKAVAEIAGFPFGS-FCNIWVAFDIMCSTASILNLCVISVDIY 123
Y 121 AICCPQLVTRNKTPLRIALMLGGCWVPTFTFISFLPDMQWNNIGIIDLERSLNQGLQD 180
b 124 AI-SSPFYERKMTKPAAFILISVANTLSVLSPFVQLSWHK-----165
Y 181 FFAIEKRKFQNSNSTCYCFVMNKPVAITCSVVAFFIPPLMLVLAAYRIYVTAKEHAHQI 240
b 183 TH-----NCDSSLSRTVAISSLSIFPIPAIMIVTVTRIVRIAQKQIRRI 228
Y 241 QMLORAGASSE-----SRPOSADQSHSTRMRTTKAATLCIIMGFCFLCW 286
b 229 SALERAHAHAKNCQTTAGNPNACQSPSSPKFMR---ETKVLKTLVINGVFCVCM 285
Y 287 APFVTVNVDPI-----DYTVGQVWTAFLWGLYNSGLNPFYAFLNKSFRRAPLII 340
b 286 LPFILNCLWMPFGSGSETKFCIDSTDFVFWFGWANSLSNPITIAF-NADFRKAFSTL 344
Y 341 LCDDERYRPSILGTVPCTTTI-----NGSTHVLDRDAVECGQWESQCH 387
b 345 LGC-----LCPTSTNAITVSNNGAAMFSSHHEPRGSIKDCN 386
```

RESULT 12

```
151661
dopamine D1C receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51661
R:Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150; PMID:7937989
A:Accession: I51661
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-465 <SUG>
A:Cross-references: EMBL:U07865; NID:g559763; PIDN:AAA50830.1; PID:g559764
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 27.2%; Score 580; DB 2; Length 465;
Best Local Similarity 39.0%; Pred. No. 1.2e-44;
Matches 130; Conservative 53; Mismatches 114; Indels 36; Gaps 7;

QY 26 LSTVILMAILGNLLVMVAVCWDRQLRKIKTYFIVSLAFADLLSVLWMPGATLVDI 85
Db 35 LSLLSLTLGLTLCVAVIRFHLRSKVTNFFVLSLAVSDLFVALLWMPKAVTEVAGF 94
QY 86 WIYGEVFCVLTSLDVLTTASIFHLCCISLDRIYAI CQPLVYRNKMTPLRIALMLGGC 145
Db 95 WVEGD-FCDTWVAFDIMCSTASILNLCIISLDRIYAI-ASPPYERKMTQVAFIMIGVA 152
QY 146 WVIPTFISFLPDMQWNNIGIIDLERSLNQGLQDFAIEKRKFQNSNSTCYCFVMNKP 205
Db 153 WTLISLISFIPVQLSWHKSHEADEE-----LNGVNHTECDSLSLNT 194
QY 206 YAITCSVVAFFIPPLMLVLAAYRIYVTAKEHAHQIOMLORAGASSE---SRPOSADQSH 262
Db 195 YAISSLSIFYPVIMIGTYTRIYIAQTQIRRISSLERAVEHAQRCSSRLSNSLSLT 254
QY 263 HRMTETKAAKTLCIIMGFCFLCWAPFFVTNIVDPIFYTVPGQ-----VWTFAP 311
Db 255 -SFRKTKVLKTLISLIMGVFVFCMLPFFVLCNMIFFCHNLPGQNEPEPCVSETTFNIF 313
QY 312 LMLGYNLSGLNPFYAFLNKSFRRAPLILCDD 344
Db 314 VWFGWANSLSNPVIYAF-NADFRKAFPTTLGCN 345

RESULT 13
A25896
beta-adrenergic receptor - turkey
C:Species: Meleagris gallopavo (common turkey)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 13-Aug-1999
C:Accession: A25896
R:Yarden, Y.; Rodriguez, H.; Wong, S.K.P.; Brandt, D.R.; May, D.C.; Burnier, J.; Harkin
Proc. Natl. Acad. Sci. U.S.A. 83, 6795-6799, 1986
A:Title: The avian beta-adrenergic receptor: primary structure and membrane topology.
A:Reference number: A25896; MUID:86313664; PMID:3018746
A:Accession: A25896
A:Molecule type: mRNA
A:Residues: 1-483 <VAR>
A:Cross-references: GB:M14379; NID:g213891; PIDN:AAA49627.1; PID:g213892
A:Experimental source: erythrocyte
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.9%; Score 574; DB 2; Length 483;
Best Local Similarity 37.0%; Pred. No. 4.5e-44;
Matches 141; Conservative 57; Mismatches 135; Indels 48; Gaps 11;

QY 26 LSTVILMAILGNLLVMVAVCWDRQLRKIKTYFIVSLAFADLLSVLWMPGATLVDI 85
Db 48 MALVLLIIVAGNVITAAIGRTQRLQTL-TNLFITSLACADLWMLLVVFPFGATLVVRC 106
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GenCore version 5.1.6
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M protein - protein search, using sw model

un on: August 5, 2004, 13:28:38 ; Search time 13 Seconds

(without alignments)
1610.169 Million cell updates/sec

file: US-10-018-257A-2

erfect score: 2133

sequence: 1 MDKLDANVSSEBGFSGVEXV.....ESQCHPPATPLVAAQPSDT 402

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Gapop 10.0 , Gapext 0.5

sarched: 141681 seqs, 52070155 residues

otal number of hits satisfying chosen parameters: 141681

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	DB ID	Description
1	2042	95.7	388	1	SH4_HUMAN Q13639 homo sapien
2	1954	91.6	388	1	SH4_CAVPO Q70528 cavia porce
3	1913	89.7	388	1	SH4_MOUSE P97288 mus musculus
4	1886	88.4	406	1	SH4_RAT Q62758 rattus norv
5	688	30.4	137	1	SH4_PIG Q29006 sus scrofa
6	610	28.6	363	1	D1DR CARAU P35406 carassius a
7	591.5	27.7	459	1	D1DR FGURU P53452 fugu rubrip
8	588.5	27.6	451	1	DADR XENLA P42289 xenopus lae
9	587	27.5	446	1	DADR DIDMA P42288 didelphis m
10	582.5	27.3	446	1	DADR_HUMAN P21728 homo sapien
11	581.5	27.3	446	1	DADR_PIG P50130 sus scrofa
12	580	27.2	465	1	DCDR_XENLA P42291 xenopus lae
13	579.5	27.2	446	1	DADR_MACMU Q77680 macaca mula
14	574	26.9	483	1	B1AR_MELGA P07700 meleagris g
15	573.5	26.9	386	1	D1DR OREMO P47800 oreochromis
16	568	26.6	463	1	D5DR FGURU P53454 fugu rubrip
17	566	26.5	418	1	B2AR_MESAU P04274 mesocricetu
18	564.5	26.5	446	1	DADR_MOUSE Q61616 mus musculus
19	563.5	26.4	477	1	DBDR_HUMAN P21918 homo sapien
20	562.5	26.4	418	1	B2AR_BOVIN Q28044 bos taurus
21	562.5	26.4	446	1	DADR_RAT P18901 rattus norv
22	562.5	26.4	475	1	DBDR_RAT P25115 rattus norv
23	562	26.3	457	1	DBDR_XENLA P42290 xenopus lae
24	559.5	26.2	415	1	B2AR_CANFA P54833 canis fami
25	559	26.2	358	1	HH2R_RAT P25102 rattus norv
26	556	26.1	415	1	B2AR_MACMU Q28509 macaca mula
27	554	26.0	467	1	B1AR_SHEEP Q28927 ovis aries
28	553	25.9	358	1	HH2R_MOUSE P97292 mus musculus
29	553	25.9	467	1	B1AR_BOVIN Q9t596 bos taurus
30	551.5	25.9	385	1	B1AR_XENLA Q42574 xenopus lae
31	550	25.8	418	1	B2AR_MOUSE P18762 mus musculus
32	550	25.8	466	1	B1AR_RAT P18090 rattus norv
33	549	25.7	466	1	B1AR_MOUSE P34971 mus musculus

ALIGNMENTS

RESULT 1

SH4_HUMAN STANDARD; PRT: 388 AA
ID SH4_HUMAN Q13639; Q96KH9; Q96K10; Q9H199; Q9NY73; Q9UBM6; Q9UBT4; Q9UE22;
AC Q13639; Q96KH9; Q96K10; Q9H199; Q9NY73; Q9UBM6; Q9UBT4; Q9UE22;
AC Q9UE23; Q9UQR6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5-hydroxytryptamine 4 receptor (5-HT4) (Serotonin receptor) (5-HT4).
GN HTR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A); 5-HT4(B); 5-HT4(C) AND 5-HT4(D)).
RC TISSUE=Gut;
RX MEDLINE=98264328; PubMed=9603189;
RA Blondel O., Gastineau M., Dahmoune Y., Langlois M., Fischmeister R.;
RT "Cloning, expression, and pharmacology of four human 5-hydroxytryptamine receptor isoforms produced by alternative splicing in the carboxyl terminus";
RT J. Neurochem. 70:2252-2261(1999).
RL [2]
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5HT4(B)).
RC TISSUE=Brain;
RA Van den Wyngaert I., Gommeren W., Jurzak M., Verhasselt P., Gordon R., Leyens J., Luyten W., Bender E.;
RT "Cloning and expression of 5-HT4 receptor species and splice variants";
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RL [3]
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(A)).
RC TISSUE=Heart;
RX MEDLINE=98012006; PubMed=9351641;
RA Claesysen S., Faye P., Sebben M., Lemaire S., Bockaert J., Dumuis A.;
RT "Cloning and expression of human 5-HT4S receptors. Effect of receptor density on their coupling to adenylyl cyclase";
RT NeuroReport 8:3189-3195(1997).
RL [4]
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(B)).
RC TISSUE=Brain;
RX MEDLINE=99238795; PubMed=10220570;
RA Claesysen S., Sebben M., Becamel C., Bockaert J., Dumuis A.;
RT "Novel brain-specific 5-HT4 receptor splice variants show marked constitutive activity: role of the C-terminal intracellular domain.";
RT Mol. Pharmacol. 55:910-920(1999).
RL [5]
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A); 5-HT4(E) AND 5-HT4(G)).
RC TISSUE=Hippocampus;
RA Vilario M.T., Domenech T., Palacios J.M., Mengod G.;
RT "Cloning and characterization of multiple human 5-HT4 receptor variants including a novel variant that lacks the alternatively spliced C-terminal exon";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL

34 548.5 25.7 332 1 TAR1_RAT Q923Y9 rattus norv
35 547.5 25.7 347 1 TAR2_RAT Q923Y7 rattus norv
36 547 25.6 413 1 B2AR_HUMAN P07550 homo sapien
37 546 25.6 338 1 TAR1_MACMU Q8hz64 macaca mula
38 545.5 25.6 359 1 HH2R_HUMAN P25021 homo sapien
39 545.5 25.6 359 1 HH2R_PANTR P60021 pan troglod
40 545.5 25.6 468 1 B1AR_PIG Q28998 sus scrofa
41 545 25.6 453 1 SHT1_APLCA Q18950 aplysia cal
42 544.5 25.5 418 1 B2AR_PIG Q28997 sus scrofa
43 543.5 25.5 418 1 B2AR_FELCA Q9tst5 felis silve
44 539.5 25.3 332 1 TAR1_MOUSE Q923Y8 mus musculus
45 539.5 25.3 428 1 B4AR_MELGA P43141 meleagris g


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Best Local Similarity 92.0%; Pred. No. 3.5e-136;
Matches 370; Conservative 8; Mismatches 10; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEGGSGVEKVVLLFLSTVILMAIIGNLLVMVAVCWDRQLRKIKTNYFIV 60
DB 1 MDKLDANVSSEGGSGVEKVVLLFLSTVILMAIIGNLLVMVAVCWDRQLRKIKTNYFIV 60
QY 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
DB 61 SLAFADLLVSVLWMPFGAIELVQDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
QY 121 ACCOPLVYRNKMTPLRLTALMGGCWVPTTISFLPIMOGWNNIGIIDLERSLNQGLGD 180
DB 121 ACCOPLVYRNKMTPLRLTALMGGCWVPTTISFLPIMOGWNNIGIIDLERSLNQGLGD 180
QY 181 FFAIEKRFNONSSTYCVFVNKYFATITCSVAFYIPFLMLVLYRYIYVYAKEHAGI 240
DB 170 ---IEKRFNONSSTYCVFVNKYFATITCSVAFYIPFLMLVLYRYIYVYAKEHAGI 226
QY 241 QMLQAGASSERPOSADQSHSTRMRTTAKATLCTIIMGFCFLCWAPFFVTNIYDPPID 300
DB 227 QVLOQAGAPAEGRPOPADQSHSTRMRTTAKATLCTIIMGFCFLCWAPFFVTNIYDPPID 286
QY 301 YVPCQVMTAFILWGLVINSGLNPFLYAFLNKSFRAFLIILCCDDERYRRPSILGQVPC 360
DB 287 YVPCQVMTAFILWGLVINSGLNPFLYAFLNKSFRAFLIILCCDDERYRRPSILGQVPC 346
QY 361 STTTINGSTHVLDRVCEGGQWESQCHPPATSPPLVAAQPSDT 402
DB 347 STTTINGSTHVLDRVCEGGQWESQCHPPATSPPLVAAQPSDT 388

RESULT 3
5H4_MOUSE STANDARD; PRT; 388 AA.
AC P97288; O89003; O89004; Q9R2A4;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 5-hydroxytryptamine 4 receptor (5-HT4) (Serotonin receptor) (5-HT4).
GN HTR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss; TISSUE=Brain;
RX MEDLINE=9102706; PubMed=8946946;
RA Claessens S., Sebben M., Journot L., Bockaert J., Dumuis A.;
RT "Cloning, expression and pharmacology of the mouse 5-HT(4L)
RT receptor."
RL FEBS Lett. 398:19-25(1996).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Dumuis A.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(E)).
RC STRAIN=Swiss; TISSUE=Brain;
RX MEDLINE=99127199; PubMed=9928238;
RA Claessens S., Faye P., Sebben M., Taviaux S., Bockaert J., Dumuis A.;
RT "5-HT4 receptors: cloning and expression of new splice variants."
RL Ann. N.Y. Acad. Sci. 861:49-56(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(F)).
RC TISSUE=Brain;
RX MEDLINE=99238795; PubMed=10220570;
RA Claessens S., Sebben M., Becamel C., Bockaert J., Dumuis A.;
RT "Novel brain-specific 5-HT4 receptor splice variants show marked
RT constitutive activity: role of the C-terminal intracellular domain."
RL Mol. Pharmacol. 55:910-920(1999).
CC -!- FUNCTION: This is one of the several different receptors for 5-

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RESULT 2

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H4_CAVPO STANDARD; PRT; 388 AA.
C 070528;
T 30-MAY-2000 (Rel. 39, Created)
T 30-MAY-2000 (Rel. 39, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E 5-hydroxytryptamine 4 receptor (5-HT4) (Serotonin receptor) (5-HT4).
N HTR4.
S Cavia porcellus (Guinea pig).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
X NCBI_TaxID=10141;
P [1]
P SEQUENCE FROM N.A.
A Van den Wyngaert I., Gommeren W., Jursak M., Verhaaselt P., Gordon R.,
A Leyssen J., Luyten W., Bender E.;
T "Cloning and expression of 5-HT4 receptor species and splice
T variants."
L Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
C -!- FUNCTION: This is one of the several different receptors for 5-
C 5-hydroxytryptamine (serotonin), a biogenic hormone that functions
C as a neurotransmitter, a hormone, and a mitogen. The activity of
C this receptor is mediated by G proteins that stimulates adenylyate
C cyclase (By similarity).
C -!- SUBCELLULAR LOCATION: Integral membrane protein.
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=1;
C Comment=A number of isoforms are produced;
C Name=1;
C IsoId=O70528-1; Sequence=Displayed;
C -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
C This SWISS-PROT entry is copyright. It is produced through a collaboration
C between the Swiss Institute of Bioinformatics and the EMBL outstation -
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
C modified and this statement is not removed. Usage by and for commercial
C entities requires a license agreement (See http://www.isb-sib.ch/announce/
C or send an email to license@isb-sib.ch).
C
C EMBL; Y13585; CAA73912.1; -
C HSP; P29274; 1MMH.
C InterPro; IPR000276; GPCR Rhodopsin.
C Pfam; PF00001; 7tm 1; 1.
C PRINTS; PR00237; GPCRHOPOPSN
C PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
C PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
C G-protein coupled receptor; Transmembrane; Glycoprotein;
C Multigene family; Lipoprotein; Palmitate; Alternative splicing.
C DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).
C TRANSMEM 20 40 1 (POTENTIAL).
C DOMAIN 41 58 CYTOPLASMIC (POTENTIAL).
C TRANSMEM 59 79 2 (POTENTIAL).
C DOMAIN 80 93 EXTRACELLULAR (POTENTIAL).
C TRANSMEM 94 116 3 (POTENTIAL).
C DOMAIN 117 137 CYTOPLASMIC (POTENTIAL).
C TRANSMEM 138 158 4 (POTENTIAL).
C DOMAIN 159 192 EXTRACELLULAR (POTENTIAL).
C TRANSMEM 193 213 5 (POTENTIAL).
C DOMAIN 214 260 CYTOPLASMIC (POTENTIAL).
C TRANSMEM 261 281 6 (POTENTIAL).
C DOMAIN 282 294 EXTRACELLULAR (POTENTIAL).
C TRANSMEM 295 315 7 (POTENTIAL).
C DOMAIN 316 388 CYTOPLASMIC (POTENTIAL).
C CARBOHYD N-DINKED (GLCNAC. . .) (POTENTIAL).
C LIPID BY SIMILARITY.
C S-palmitoyl cysteine (By similarity).
C SEQUENCE 388 AA; 43725 MW; 3D45B3A37F6D02B CRC64;
Query Match 91.6%; Score 1954; DB 1; Length 388;

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hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylyate cyclase (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;

Name=1;

isoId=P97288-1; Sequence=Displayed;

Name=5-HT4(A);

isoId=P97288-2; Sequence=VSP_001851;

Name=5-HT4(E);

isoId=P97288-3; Sequence=VSP_001852;

Name=5-HT4(F);

isoId=P97288-4; Sequence=VSP_001853;

-!- SIMILARITY: Belongs to family I of G-protein coupled receptors.

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EMBL; Y09585; CAA70773.1; -;

EMBL; Y09587; CAA70775.1; -;

EMBL; Y09588; CAA70776.1; -;

EMBL; AJ011369; CAA09598.1; -;

HSSP; P29274; 1WQH.

MGI; MGI:109246; Hcr4.

InterPro; IPR000276; GPCR Rhodspan.

Pfam; PF00001; 7tm.1; 1.

PRINTS; PR00237; GPCRHHODPSN.

PROSITE; PS00237; G PROTEIN RECP FL 1; 1.

PROSITE; PS00262; G PROTEIN RECP FL 2; 1.

PROSITE; PS0262; G PROTEIN RECP FL 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;

Multi-gene family; Lipoprotein; Palmitate; Alternative splicing.

FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 20 40 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 41 58 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 59 79 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 80 93 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 94 116 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 117 137 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 138 158 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 159 192 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 193 213 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 214 260 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 261 281 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 282 294 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 295 315 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 316 388 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 7 7 BY SIMILARITY.

FT DISULFID 93 184 S-palmitoyl cysteine (By similarity).

FT LIPID 329 329 DAVECGQWESRCHLTATPLVAAQPSDT -> YTVLHSGH

FT VARSP LIC 360 388 HQEKLPIHNDPESLESCF (in isoform 5-HT4(A)).

FT FTId=VSP_001851.

FT VARSP LIC 359 388 RDAVECGQWESRCHLTATPLVAAQPSDT -> SFPLLF

FT NRPV (in isoform 5-HT4(E)).

FT FTId=VSP_001852.

FT VARSP LIC 360 388 DAVECGQWESRCHLTATPLVAAQPSDT -> PVFV (in isoform 5-HT4(F)).

FT FTId=VSP_001853.

FT SEQUENCE 388 AA; 43931 MW; F84163F39B4115B0 CRC64;

Query Match 89.7%; Score 1913; DB 1; Length 388;

Best Local Similarity 90.3%; Pred. No. 3.5e-133;

Matches 363; Conservative 11; Mismatches 14; Indels 14; Gaps 1;

QY 1 MDKLDANVSSEEGFSGVERKVVLLTFLAVIIMAILGNLVMVAVCDRLKIKTNFYIV 60

Db 1 MDKLDANVSSEEGFSGVERKVVLLTFLAVIIMAILGNLVMVAVCDRLKIKTNFYIV 60

QY 61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDYY 120

Db 61 SLAFADLLVSVLWMPFGAIELVDQIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDYY 120

QY 121 AICCOPLVYRNKMTPLRIALMLGGCWIPITFISFLPMQGNWNIIGIDLSRLNQGLQD 180

Db 121 AICCOPLVYRNKMTPLRIALMLGGCWIPITFISFLPMQGNWNIIGIDLSRLNQGLQD 180

QY 181 FHATEKRFKNSNSTCYFVFNKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAQI 240

Db 170 ---TEKRFKNSNSTCYFVFNKPYAITCSVAFYIPFLMLVLAIRIYVTAKEHAQI 226

QY 241 QMLORAGASSSRPOSADQSHTRMRTETKAATLCIIMGCFCLCWAPFFVTNVDPPID 300

Db 227 QMLORAGASSSRPOSADQSHTRMRTETKAATLCIIMGCFCLCWAPFFVTNVDPPID 286

QY 301 YTVPGQWTAFLMGLYNSGLNPFYAFNLSFRFRAFLIILCCDDRYRRPSIIGQTVPC 360

Db 287 YTVPGQWTAFLMGLYNSGLNPFYAFNLSFRFRAFLIILCCDDRYRRPSIIGQTVPC 346

QY 361 STTTINGSTHYLRDAVECGQWESQCHPPATSPVAAQPSDT 402

Db 347 STTTINGSTHYLRDAVECGQWESRCHLTATSPVAAQPSDT 388

RESULT 4

SH4_RAT STANDARD; PRT; 406 AA.

ID SH4_RAT

AC Q62758; O89034; Q62757; Q63006;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 5-hydroxytryptamine 4 receptor (5-HT₄) (Serotonin receptor) (5-HT₄).

GN HTR4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=95317299; PubMed=7796807;

RA Gerald C., Adham N., Kao H.T., Olsen M.A., Laz T.M., Schechter L.E., Bard J.A., Vaysses P., Hartig P.R., Branchek T.A., Weinschenk R.L.; "The 5-HT₄ receptor: molecular cloning and pharmacological characterization of two splice variants.";

RT Characterization of two splice variants.";

RL EMBO J. 14:2806-2815(1995).

RN [2]

RP SEQUENCE OF 165-259 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=95385798; PubMed=7656980;

RA Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.; "Expression of serotonin receptor mRNAs in blood vessels.";

RL FEBS Lett. 370:215-221(1995).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(E)).

RC TISSUE=Brain;

RX MEDLINE=95220570; PubMed=10220570;

RA Claeysen S., Sebben M., Becamel C., Bockaert J., Dumuis A.; "Novel brain-specific 5-HT₄ receptor splice variants show marked constitutive activity: role of the C-terminal intracellular domain.";

RL Mol. Pharmacol. 55:910-920(1999).

CC -!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylyate cyclase.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

Comment=Additional isoforms seem to exist;
 Name=5-HT4L;
 IsoId=Q62758-1; Sequence=Displayed;
 Name=5-HT4S;
 IsoId=Q62758-2; Sequence=VSP_001854;
 Name=5-HT4(E);
 IsoId=Q62758-3; Sequence=VSP_001855;
 -!- TISSUE SPECIFICITY: In brain, the 5-HT4S transcripts are restricted to the striatum, but the 5-HT4L transcripts are expressed throughout the brain, except in the cerebellum. In peripheral tissues, differential expression is also observed in the atrium of the heart where only the 5-HT4S isoform is detectable.
 -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 EMBL; U20907; AAC52233.1; -;
 EMBL; U20906; AAC52232.1; -;
 EMBL; Z48153; CAA88170.1; -;
 EMBL; AJ011370; CAA09599.1; -;
 PIR; S55549; S55549.
 PIR; S55549; S55549.
 HSSP; P29274; 1MMH.
 InterPro; IPR000276; GPCR_Rhodpsn.
 Pfam; PF00001; 7tm.1; 1.
 PRINTS; PR00237; GPCRHOPOPSN.
 PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Alternative splicing; Lipoprotein; Palmitate.
 DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 20 40 1 (POTENTIAL).
 DOMAIN 41 58 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 59 79 2 (POTENTIAL).
 DOMAIN 80 93 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 94 116 3 (POTENTIAL).
 DOMAIN 117 137 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 138 158 4 (POTENTIAL).
 DOMAIN 159 192 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 193 213 5 (POTENTIAL).
 DOMAIN 214 260 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 261 281 6 (POTENTIAL).
 DOMAIN 282 294 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 295 315 7 (POTENTIAL).
 DOMAIN 316 406 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 LIPID 93 184 S-palmitoyl cysteine (By similarity).
 LIPID 329 329 DIVECGQWESRCHLATSPLVAQPVIRRPQNDLEDSCS
 VARSPLIC 360 406 LKQSQS -> YTVLHGQHQEKLPHINDPESLESCF (in isoform 5-HT4S).
 VARSPLIC 359 406 RDTVECGQWESRCHLATSPLVAQPVIRRPQNDLEDSC (in isoform 5-HT4S).
 SLEKQSQS -> SPFLFCNRPVPV (in isoform 5-HT4(E)).
 FTIG-VSP_001855.
 NA -> MP (IN REF. 3).
 CONFLICT 74 75
 SEQUENCE 406 AA; 46107 MW; A1889155A0893084 CRC64;
 Query Match 88.4%; Score 1886; DB 1; Length 406;
 Best Local Similarity 89.5%; Pred. No. 3.4e-131;
 Matches 357; Conservative 12; Mismatches 16; Indels 14; Gaps 1;
 1 MOKLDANVSSEGFSGVEKVLTLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNYFTV 60
 1 MDELNDANVSNEGFGSVEKVLTLTFFAMVILMAILGNLLVMVAVCDRLRKIKNYFTV 60

61 SLAFADLLVSVLWMPFGAIELVDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
 61 SLAFADLLVSVLVNAFAGIELVDIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRIY 120
 121 AICCCPLVYRNKMTLRALMLGGCWVLPTRISFLPIMQGNWNIIGIDILERSLNQGLQD 180
 121 AICCCPLVYRNKMTLRALMLGGCWVLPTRISFLPIMQGNWNIIGIDV- 169
 181 FIAIEKRRFPNNSNSTYCVFVWVKNKEVATCSVAFYIPFLMLVLAAYRIYVTAKEHAQI 240
 170 ---IEKRRFNNSNSTPFCVWVKNKEVATCSVAFYIPFLMLVLAAYRIYVTAKEHAQI 226
 241 QMLRAGASSRSRPOSADOSHTRMRTETKAATLCIIMGCFCPCWAPFFVTNIVDPFID 300
 227 QMLRAGATSESRPOTADQSHTRMRTETKAATLCVIMGCFCPCWAPFFVTNIVDPFID 286
 301 YTVPGQVATFALMLGVIYNSGLNPLFYAFLNKSFRAFLIILCCDDRYRRBSILGQTVPC 360
 287 YTVPGQVATFALMLGVIYNSGLNPLFYAFLNKSFRAFLIILCCDDRYRRBSILGQTVPC 346
 361 STTTINGSTHVLDRAVECGQWESQCHPPATSPVLAQOP 399
 347 STTTINGSTHVLDRIVECGQWESRCHLTATSPVLAQOP 385
 RESULT 5
 5H4_PIG
 ID 5H4_PIG STANDARD; PRT; 137 AA.
 AC Q2906;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 5-hydroxytryptamine 4 receptor (5-HT-4) (Serotonin receptor) (5-HT4) (Fragment).
 GN HTR4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95385798; PubMed=7656980;
 RA Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
 RT "Expression of serotonin receptor mRNAs in blood vessels.";
 RL FEBS Lett. 370:215-221(1995).
 CC -!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylyate cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 EMBL; Z48175; CAA88198.1; -;
 PIR; S66487; S66487.
 InterPro; IPR000276; GPCR_Rhodpsn.
 Pfam; PF00001; 7tm.1; 1.
 PRINTS; PR00237; GPCRHOPOPSN.
 PROSITE; PS00237; G PROTEIN RECP F1.1; PARTIAL.
 PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
 NON_TER 1

T the puffer fish *Fugu rubripes*.";
 L Genomics 25:436-446(1995).
 C -!- FUNCTION: Receptor for dopamine.
 C -!- SUBCELLULAR LOCATION: Integral membrane protein.
 C -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 C -----
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 C entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 C or send an email to license@isb-sib.ch).
 C -----
 C EMBL; X80174; CAA56455.1; -;
 C FIRM; A56849; A56849.
 C InterPro; IPR000276; GPCR_Rhodpsn.
 C Pfam; PF00001; 7tm.1.1.
 C PRINTS; PR00237; GPCRHOOPS.
 C PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
 C PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
 C G-protein coupled receptor; Transmembrane; Glycoprotein;
 C Multigene family.
 C T DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 24 49 1 (POTENTIAL).
 C T DOMAIN 50 60 CYTOPLASMIC (POTENTIAL).
 C T TRANSMEM 61 87 2 (POTENTIAL).
 C T DOMAIN 88 96 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 97 119 3 (POTENTIAL).
 C T DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).
 C T TRANSMEM 139 164 4 (POTENTIAL).
 C T DOMAIN 165 191 1 (POTENTIAL).
 C T TRANSMEM 192 216 5 (POTENTIAL).
 C T DOMAIN 217 269 CYTOPLASMIC (POTENTIAL).
 C T TRANSMEM 270 297 6 (POTENTIAL).
 C T DOMAIN 298 311 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 312 333 7 (POTENTIAL).
 C T DOMAIN 334 459 CYTOPLASMIC (POTENTIAL).
 C T CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 C T DISULFID 96 187 BY SIMILARITY.
 C Q SEQUENCE 459 AA; 51080 MW; B69857A3A4E410B CRC64;
 C -----
 C Query Match 27.7%; Score 591.5; DB 1; Length 459;
 C Best Local Similarity 37.0%; Pred. No. 2.4e-36;
 C Matches 130; Conservative 60; Mismatches 114; Indels 47; Gaps 9;
 C -----
 C Y 16 SVEKVVLLFLSVILMAILGNLLVMVAVCWDRQLRKIKNTYFVSLAPADLLVSLVNP 75
 C b 20 SSKRVLTGCFSLSLIFLTLLGNLTLCVAVTKFHLRSKVTNFFVLSLSDLLVAILNP 79
 C Y 76 FGAIELVDIWIYGEVFCVLRISLDVLLTASIFHLCCISLDYVAICQPLVYRNKMT 135
 C b 80 WKAATEIMGFWPPE-FCNIWAFDIMCSTASILNLCVISVDYRWAI-SSPFYERKMT 137
 C Y 136 LRALMLGSCWIPITPSILPIMQGNNTGIDLSRLNGLQGDQPHATEKRFKNQNS 195
 C b 138 KVACLMISVAWTLVSLISIPVQLNW-----HKAQTASYE-LNG 176
 C Y 196 TV-----CVFMVKNPKYATCSVVAFIPVLPMLVAYRIYVTAKEBAHQIQLORAG 247
 C b 177 TVAGDLPPNCDSLSLNTVAISSLSISFIPVAIMIVTVYRIYTRAQKIRISALERAA 236
 C Y 248 ASSESPPQ-----SADQSHTRM--RTETKAATLCIIMGFCFLCWAPFFVTVNVDPP 299
 C b 237 EGAQNRHSSMGNSLSMESECSFMSKRETKVLKTLVIMGVFVCCWLPFFILNCWVPC 296
 C Y 300 DY-----TVPCQWTFALWGLYNSGLNPFLYAFLNKSFRAFLILCC 343
 C b 297 EADDTTDFPCISSTTDFVFWFGWANSLSNPIYAF-NADFRKAFSILG 346

RESULT 8
 ADR_XENLA

ID DADR XENLA STANDARD; PRT; 451 AA.
 AC P42289;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE D(1A) dopamine receptor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoides; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95024150; PubMed=7937989;
 RA Sugamori K.S.; Demchyshyn L.L.; Chung M.; Miznik H.B.;
 RT "DiA, DiB, and DiC dopamine receptors from *Xenopus laevis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10536-10540(1994).
 CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
 CC for dopamine. The activity of this receptor is mediated by G
 CC proteins which activate adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 C or send an email to license@isb-sib.ch).
 C -----
 C EMBL; U07863; AAA50828.1; -;
 C FIRM; I51659; I51659.
 C InterPro; IPR000276; GPCR_Rhodpsn.
 C Pfam; PF00001; 7tm.1.1.
 C PRINTS; PR00237; GPCRHOOPS.
 C PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
 C PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
 C G-protein coupled receptor; Transmembrane; Glycoprotein;
 C Multigene family; Lipoprotein; Palmitate.
 C T DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 23 48 1 (POTENTIAL).
 C T DOMAIN 49 59 CYTOPLASMIC (POTENTIAL).
 C T TRANSMEM 60 86 2 (POTENTIAL).
 C T DOMAIN 87 95 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 96 118 3 (POTENTIAL).
 C T DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
 C T TRANSMEM 138 162 4 (POTENTIAL).
 C T DOMAIN 163 191 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 192 217 5 (POTENTIAL).
 C T DOMAIN 218 271 CYTOPLASMIC (POTENTIAL).
 C T TRANSMEM 272 298 6 (POTENTIAL).
 C T DOMAIN 299 315 EXTRACELLULAR (POTENTIAL).
 C T TRANSMEM 316 340 7 (POTENTIAL).
 C T DOMAIN 341 451 CYTOPLASMIC (POTENTIAL).
 C T CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 C T DISULFID 95 185 BY SIMILARITY.
 C T LIPID 350 350 S-palmitoyl cysteine (By similarity).
 C Q SEQUENCE 451 AA; 50549 MW; 3A0F8AB36C166687 CRC64;
 C -----
 C Query Match 27.6%; Score 588.5; DB 1; Length 451;
 C Best Local Similarity 34.5%; Pred. No. 3.8e-36;
 C Matches 146; Conservative 64; Mismatches 150; Indels 63; Gaps 13;
 C -----
 C Y 16 SVEKVVLLT-----FLSVILMAILGNLLVMVAVCWDRQLRKIKNTYFVSLA 63
 C b 7 SMDDEVLLTERESSPRVLTGCFSLVLLISLTLLGNLTLCVCAVIRFHLRSKVTNFFVLSLA 66
 C Y 64 PADLLVSVLWVPFGAIELVDIWIYGEVFCVLRISLDVLLTASIFHLCCISLDYVAIC 123
 C b 67 VSDLLVAVLWPKVAELIAGFWPPEG-TFCNIWAFDIMCSTASILNLCVISVDYRWAI- 124

QY 124 CQPLVTRNMTPLRIALMLGGCWVITPFIISFIPIMQGN---NIGIIDLSRINQGLQD 180
 Db 125 SSPFRYERKMTPKVAFIMIGVATWLVLSIFIPVQLNMHKAKTSPFDLNLTLH----- 178
 QY 181 FHAIEKKFNQNSNTCYFVFNKPAITCSVVARVIFPFLMLVLAAYRIYVTAKEHAHQI 240
 Db 179 -----DRTMDCDSSLNRTYIAISSLSFIPVAIMIVITRIYRIANAKQIRRI 227
 QY 241 QMLQRA-----SSSRPQAD-QHSTRMRT-----ETKAAKTLICIMGFCCLCWAPP 289
 Db 228 SALERAHVAKONCONSTNRNSLDCCQPESSLKTSFKETKVLKTLVSGVGVCCWLPF 287
 QY 290 FVTNIVDPID-----YVPCQVWTAFLWGLYINSGLNPLFIYAFNKSFRAPFLI 339
 Db 288 FILNCIVPCDFSLTSTGTEPFCSITSTTFDVFVFWGANSNLPIIYAF-NADPRKAFSN 346
 QY 340 ILCCDDERYRRPSILGQVPCSTTTINGSTHVLDA-VECGQWESQCHPPATSPILVAAQ 398
 Db 347 LIGC-----YRLCPTSNII--ETVSINNGAVVYSCQEPKGSIPNECNLVYLIPHATIC 400
 QY 399 PSD 401
 Db 401 PED 403

RESULT 9

DADR DIDMA STANDARD; PRT; 446 AA.
 AC P42288;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE D(1A) dopamine receptor.
 GN DRD1.
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=94067048; PubMed=8246914;
 RA Nash S.R., Godinot N., Caron M.G.;
 RT "Cloning and characterization of the opossum kidney cell D1 dopamine
 RT receptor: expression of identical D1A and D1B dopamine receptor mRNAs
 RT in opossum kidney and brain."
 RL Mol. Pharmacol. 44:918-925(1993).
 CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors
 CC for dopamine. The activity of this receptor is mediated by G
 CC proteins which activate adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL; S67258; AAB29143.1; -
 DR InterPro; IPR000276; GPCR Rhodopsin.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 23 48 1 (POTENTIAL).
 FT DOMAIN 49 59 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 60 86 2 (POTENTIAL).
 FT

FT DOMAIN 87 95
 FT TRANSMEM 96 118
 FT DOMAIN 119 137
 FT TRANSMEM 138 162
 FT DOMAIN 163 191
 FT TRANSMEM 192 217
 FT DOMAIN 218 271
 FT TRANSMEM 272 298
 FT DOMAIN 299 315
 FT TRANSMEM 316 340
 FT DOMAIN 341 446
 FT CARBOHYD 4 4
 FT DISULFID 95 185
 FT LIPID 350 350
 FT LIPID 354 354
 SQ SEQUENCE 446 AA; 49761 MW; A6B1FF3CBF6476C CRC64;
 Query Match 27.5%; Score 587; DB 1; Length 446;
 Best Local Similarity 34.8%; Pred. No. 4.9e-36;
 Matches 143; Conservative 69; Mismatches 145; Indels 54; Gaps 13;
 QY 1 MDKLDANVSSEEGFSGVEKVVLLTFLSTVILMAILNLLVMVAVCWDRQLKIKNTYFIV 60
 Db 8 MDRRLGVVERDFSP-----RIITACFLSLILLSTLGLNTLVCAAVIRFRLRSKVTNFEVI 63
 QY 61 SLAFADLLSVLVNPPGAIELVQDIWIYGEVFCVTRTSLDVLTLTASTFHLCCISLDRY 120
 Db 64 SLAVSDLLAVLVNPPGKAVAEIAGFWPFGS-FCN1WVAFD1MCSTASILNLCVISVDQY 122
 QY 121 AICQPLVYRNKMTPLRIALMLGGCWVITPFIISFIPIMQGNIIIDLSRINQGLQD 180
 Db 123 AI-SSPFRYERKMTPKVAFIMIGVATWLVLSIFIPVQLNMHK-----ARPLSSPDG-- 173
 QY 181 FHAIEKKFNQNSNTCYFVFNKPAITCSVVARVIFPFLMLVLAAYRIYVTAKEHAHQI 240
 Db 174 -----NVSSQDETMDNCSSLSRTYIAISSLSFIPVAIMIVITRIYRIANAKQIRRI 227
 QY 241 QMLQRA-----GASSE-SRPOSADQSHTRMRTETTKAATLCIIMGFCCLCW 286
 Db 228 SALERAHVAKONCONTTNGANVECSQPESSFKR---ETVKLTSLVSGVGVCCW 284
 QY 287 APFFVTNIVDPIDVTPV-GO-----VMTAFMLGYNGLNPLFIYAFNKSFRRA 336
 Db 295 LPFILNCVWPFCESDLPSTGKPKFCIDSTFDVFWFGWANSNLPIIYAF-NADPRKA 343
 QY 337 FLIILCCDDERYRRPSILGQVPCSTTTINGSTHVLDAVECGQWESQCH 387
 Db 344 FSTLLGC-----YRLCPTANNAI--ETVSINNGAVFSSHHBPRGSISKDCN 388
 RESULT 10
 DADR HUMAN STANDARD; PRT; 446 AA.
 AC P21728;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE D(1A) dopamine receptor.
 GN DRD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90370093; PubMed=2144334;
 RA Dearth A., Gingrich J.A., Falardeau P., Fremerey R.T. Jr., Bates M.D.,
 RA Caron M.G.;
 RT "Molecular cloning and expression of the gene for a human D1 dopamine
 RT receptor."
 RL Nature 347:72-76(1990).
 RN [2]
 RP SEQUENCE FROM N.A.

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M protein - protein search, using sw model

run on: August 5, 2004, 13:32:29 ; Search time 39 Seconds
(without alignments)

3252.265 Million cell updates/sec

title: US-10-018-257A-2

effect score: 2133

sequence: 1 MDKLDANSSBEGFGVEKV.....ESQCHPPATSPILVAAQPSDT 402

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1017041 seqs, 315518202 residues

total number of hits satisfying chosen parameters: 1017041

inimum DB seq length: 0

aximum DB seq length: 2000000000

Opt-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

SPREMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rviro.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	2038	95.5	388	4 Q81XH9	Q81XH9 homo sapien
2	1879	88.1	387	4 Q96X10	Q96X10 homo sapien
3	700	32.8	151	6 Q29007	Q29007 sus scrofa
4	599	28.1	437	13 Q42316	Q42316 cyprinus ca
5	598.5	28.1	388	5 Q8MTW6	Q8MTW6 episcula sol
6	598.5	28.1	508	5 Q9VCZ3	Q9VCZ3 drosophila
7	593	27.8	446	13 Q42315	Q42315 cyprinus ca
8	591	27.7	445	13 Q98842	Q98842 anguilla an
9	585.5	27.4	418	11 Q8K424	Q8K424 cavia porce
10	581	27.2	445	13 Q98841	Q98841 anguilla an
11	580	27.2	446	6 Q8WND7	Q8WND7 bos taurus
12	569	26.7	448	13 Q98844	Q98844 anguilla an
13	564	26.4	458	13 Q98843	Q98843 anguilla an
14	563.5	26.4	477	4 Q8NQ8	Q8NQ8 homo sapien
15	562	26.3	391	5 Q96716	Q96716 branchiost
16	556	26.1	394	5 Q9NHf3	Q9NHf3 alypsia cal

ALIGNMENTS

RESULT 1

Q81XH9 PRELIMINARY; PRT; 388 AA.
AC Q81XH9
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE 5-hydroxytryptamine 4 receptor subunit b.
GN HTR4B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RA Bruss M.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RA Bruss M., Bonisch H.;
RT "Molecular cloning and pharmacological characterization of human 5-HT4-like receptors."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ519673; CAD58392.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00217; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 388 AA; 43789 MW; 7FCD81F0E7BDF560 CRC64;

Query Match 95.5%; Score 2038; DB 4; Length 388;

Best Local Similarity 96.3%; Pred. No. 1.3e-190; Matches 387; Conservative 1; Mismatches 0; Indels 14; Gaps 1;	
QY 1 MDKLDANVSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60	Db 1 MDKLDANVSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
Db 1 MDKLDANVSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60	QY 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120
QY 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120	Db 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120
Db 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120	QY 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180
QY 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180	Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180
Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180	QY 181 PHAIEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 240
QY 181 PHAIEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 240	Db 170 ---IEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 226
Db 170 ---IEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 226	QY 241 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 300
QY 241 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 300	Db 227 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 286
Db 227 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 286	QY 301 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 360
QY 301 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 360	Db 287 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 346
Db 287 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 346	QY 361 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 402
QY 361 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 402	Db 347 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 388
Db 347 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 388	
RESULT 2	
Q96K10 PRELIMINARY; PRT; 387 AA.	
AC Q96K10; 01-DEC-2001 (Tremblrel. 19, Created)	AC Q96K10; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)	DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)	DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE 5-hydroxytryptamine4 receptor.	DE 5-hydroxytryptamine4 receptor.
GN HTR4.	GN HTR4.
OS Homo sapiens (Human).	OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;	OX NCBI_TaxID=9606;
RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC TISSUE=Brain;	RC TISSUE=Brain;
RA Vilario M.T., Domenech T., Palacios J.M., Mengod G.;	RA Vilario M.T., Domenech T., Palacios J.M., Mengod G.;
RT "Cloning and characterization of multiple human 5-HT4 receptor	RT "Cloning and characterization of multiple human 5-HT4 receptor
RT variants including a novel variant that lacks the alternatively	RT variants including a novel variant that lacks the alternatively
RT spliced C-terminal exon."	RT spliced C-terminal exon."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; A0278979; CAC22248.1; --	DR EMBL; A0278979; CAC22248.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.	DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.	DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.	DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.	DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.	DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.	DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.	DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.	DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.	DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.	KW G-protein coupled receptor; Receptor; Transmembrane.
QY SEQUENCE 387 AA; 44109 MW; 43019BED75AC3D0F CRC64;	QY SEQUENCE 387 AA; 44109 MW; 43019BED75AC3D0F CRC64;
Query Match 88.1%; Score 1879; DB 4; Length 387;	
Best Local Similarity 95.7%; Pred. No. 4.5e-175;	
Matches 360; Conservative 0; Mismatches 2; Indels 14; Gaps 1;	
QY 1 MDKLDANVSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60	Db 1 MDKLDANVSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60
Db 1 MDKLDANVSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNFYIV 60	QY 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120
QY 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120	Db 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120
Db 61 SLAPADLLSVLVMPFGAIELVQDIWIYGEVFCVLRVSLDVLTTASIFHLCCISLDRIY 120	QY 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180
QY 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180	Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180
Db 121 AICCOPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 180	QY 181 PHAIEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 240
QY 181 PHAIEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 240	Db 170 ---IEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 226
Db 170 ---IEKRKNQNSSTYCVFMVKNPYAITCSVVAFYIPFLMVLAYRIYVTAKEHAHQI 226	QY 241 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 300
QY 241 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 300	Db 227 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 286
Db 227 QMLQRAGASSESRPOSADQSHRMTETKAATLCIIMGCFCLWAPFFVTNIVDPFID 286	QY 301 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 360
QY 301 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 360	Db 287 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 346
Db 287 YTVPGQVMTAFVLWGLYNSGLNPFYAFNLKSFRRFRAFLIILCCDDERYRRPSILGQTVP 346	QY 361 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 402
QY 361 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 402	Db 347 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 388
Db 347 STTTINGSTHVLDAVECCGOWESCHPPATPLVAAPSDT 388	
RESULT 3	
Q29007 PRELIMINARY; PRT; 151 AA.	
AC Q29007; 01-NOV-1996 (Tremblrel. 01, Created)	AC Q29007; 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)	DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)	DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Serotonin 4A receptor (5-HT4A) (Fragment).	DE Serotonin 4A receptor (5-HT4A) (Fragment).
GN 5-HT4A.	GN 5-HT4A.
OS Sus scrofa (Pig).	OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;	OX NCBI_TaxID=9823;
RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC TISSUE=Coronary artery;	RC TISSUE=Coronary artery;
RA Lubbert H.;	RA Lubbert H.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.	RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]	RN [2]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC TISSUE=Coronary artery;	RC TISSUE=Coronary artery;
RX MEDLINE=95385798; PubMed=7656980;	RX MEDLINE=95385798; PubMed=7656980;
RT Ulmer C., Schmuck K., Kalkman H.O., Lubbert H.;	RT Ulmer C., Schmuck K., Kalkman H.O., Lubbert H.;
RT "Expression of serotonin receptor mRNAs in blood vessels."	RT "Expression of serotonin receptor mRNAs in blood vessels."
RL FEBS Lett. 370:215-221(1995).	RL FEBS Lett. 370:215-221(1995).
DR EMBL; Z48176; CAA88199.1; --	DR EMBL; Z48176; CAA88199.1; --
DR PIR; S66495; S66495.	DR PIR; S66495; S66495.
DR GO; GO:0016021; C:integral to membrane; IEA.	DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.	DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.	DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.	DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.	DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.	DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.	DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.	DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.	DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.	KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 151 151	FT NON TER 151 151
FT NON TER 151 151	FT NON TER 151 151
SQ SEQUENCE 151 AA; 17240 MW; 6505B7CB46328750 CRC64;	SQ SEQUENCE 151 AA; 17240 MW; 6505B7CB46328750 CRC64;
Query Match 32.8%; Score 700; DB 6; Length 151;	
Best Local Similarity 85.4%; Pred. No. 2.5e-60;	
Matches 129; Conservative 8; Mismatches 14; Indels 0; Gaps 0;	
QY 123 CCQPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 182	Db 123 CCQPLVYRNKMTPLRIALMLGGCWVPTFISFLPMQGNWNIIDILERSLNQGLQD 182


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1 CCPLVYRNKMTPLKAVALLAGCAIPVLISFLPLMQGNNIGITLDRTSKPRGLQDLH 60
183 AIEKKEKFNQNSSTYCVPMNKPAYITCSVVAFYIPFLMLVAYRYIYVTAKEHAHQIOM 242
61 VIEKKEKFNQNSSTYCVPMNKPAYITCSVVAFYIPFLMLVAYRYIYVTAKEHAHQIOM 120
243 LORAGASSESRPOSADQSHTRMTETKAOK 273
121 LORAGAPAEGRPPSADQSHTRMTETKAOK 151

RESULT 4
12316 ID Q8MTW6 PRELIMINARY; PRT; 437 AA.
O42316;
O42316;
O1-JAN-1998 (Tremblrel. 05, Created)
O1-JAN-1998 (Tremblrel. 05, Last sequence update)
O1-JUN-2003 (Tremblrel. 24, Last annotation update)
D1A4 dopamine receptor.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
[1]
SEQUENCE FROM N.A.
TISSUE=Retina;
MEDLINE=99044151; PubMed=9826915;
Hirano J., Archer S.N., Djangoz M.B.A.;
"Dopamine receptor subtypes expressed in vertebrate (carp and eel)
retinae: cloning, sequencing and comparison of five D1-like and three
D2-like receptors."
Recept. Channels 5:387-404(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; V14627; CAA74971.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHOPOPSN
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 437 AA; 48707 MW; A44749475P2139CE CRC64;

Query Match 28.1%; Score 599; DB 13; Length 437;
Best Local Similarity 35.7%; Pred. No. 6.2e-50;
Matches 142; Conservative 63; Mismatches 135; Indels 58; Gaps 10;

Y 4 LDANVSSEGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKNTYFI 63
9 LSSVSQR---NSSKVLTCGLSLILLTLLGNTLVCAVTKFHLRSKVTNFFVISLA 65
64 FADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRYAIC 123
66 ISDLLVAILLMPWKAASEIVGEWPFQ-AFCDVVAAPDIMCSTASILNLCVISVDRTYAI- 123
124 CQPLVYRNKMTPLRIALMLGGCVIPTFISFLPIMQGNNGIIGIDLERSLNQGLQDFHA 183
124 SGFFRYERKMTPKVAPIMSLAWTSLISLISFIPVQLNWH----- 162
184 IEKKEKFNQNSSTY-----CVFMNKPAYITCSVVAFYIPFLMLVAYRYIYVTAKEH 236
163 ----KAQAEINGTYGLPDCDSSLNRYIATSSLSIFVPAIMLVYTRIYRIAQKQ 218
237 AHQIQMLQAGASSESRPO-----SADQSHTRM--RTETKAOKTLCIIMGCFCLCWAP 288
219 IRRISALERAESAQRHSSMGNNASMESESPKMSFKRETIVKLTSLVINGVYVCCMLP 278
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289 FFVTNIVDPFID-----YTPQGVWTAFLWGLYINSLNPLFLYAFLNKSFRRALII- 340
279 FVVLNCPWPCFNWEGSDFFCISSTTDFVFWFWGANSNLPIIYAP-NAGFRKAFSILL 337
341 ----LCDDERYRPSILGQVPCSTTTINGSTHVLRD 374
338 GCHRLCPGSAIEIVSINNGGPPSTQYQPKGHVPKE 375

RESULT 5
Q8MTW6 ID Q8MTW6 PRELIMINARY; PRT; 388 AA.
AC Q8MTW6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
OS Spisula solidissima (Atlantic surf-clam).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Mactroidea; Mactridae; Spisula.
NCBI_TaxID=6584;
[1]
SEQUENCE FROM N.A.
Dube F., Legault S.;
"Putative surf clam G-protein coupled receptor.";
Submitted (SEP-2001) to the EMBL/GenBank/DBAJ databases.
EMBL; AY055377; AAL23575.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHOPOPSN
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
Receptor.
SEQUENCE 388 AA; 44383 MW; C65E8AP910447347 CRC64;

Query Match 28.1%; Score 598.5; DB 5; Length 388;
Best Local Similarity 39.9%; Pred. No. 6.1e-50;
Matches 141; Conservative 51; Mismatches 122; Indels 39; Gaps 8;

Y 4 LDANVSSEGFSGVEKVVLLTFLSTVILM---AIGNLLVMVAVCWDRQLRKIKNTYFI 59
18 LNESVVGNETTPKVE-YLLIAIKSTAMLLIMLGAIFGNILVTVAMKFERLSAINTYFI 76
60 VSLAFADLLSVLMPFGAIELVQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRY 119
77 VSLAFADFLVLSILVMPFNASTAISGKWMFGRTMCDVFNNDVLPSTASILHLCCISMDRY 136
120 YAICCQPLVYRNKMTPLRIALMLGGCVIPTFISFLPIMQGNNGIIGIDLERSLNQGLQ 179
137 IAI-IHPFKYQSKMTHFRVYVYIAITWISSILISYIPIQSHWY-----TSD 182
180 DFHATEKKEKFNQNSSTYCVFMNKPAYITCSVVAFYIPFLMLVAYRYIYVTA----- 233
183 TLKVAERPD-----CLFVNKAYAVSSSISFIPCTIMVYVYLYKIWEARQEKQ 235
234 -KEHAHQIQLQAGASSESRPOSADQSHTRMTETKAOKTLCIIMGCFCLCWAPFP-- 290
236 IKQSGVHIKELSPSEQTNLTDDQSENREKMRREHKAATGLIIMGAFVFCPLPFTW 295
291 --VTNIVDPFIDYTPQGVWTAFLWGLYINSLNPLFLYAFLNKSFRRALII 341
296 YLVVTLTCDGACP--PEMVGAACFNLGYFNCLNPIIYAYFNDRFGRAPKLL 346

RESULT 6
Q9VCZ3 ID Q9VCZ3 PRELIMINARY; PRT; 508 AA.
AC Q9VCZ3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
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QY 185 EKRKFQNGNSTVCVPMNKPVAITCSVVAFYIPFLMLVAYRYVYVTAKEHAHQIOMLO 244
DB 178 HKDAINCYAEETCCDFTNQAVAIASSIVSPFLPLVMVYVTSRVFQVAKK---QIQKID 234
QY 245 RAGASESPQS---ADQSHSTRM---TETKAATLCIIMGCFCLCWAPFFVTNI 294
DB 235 RSEGRPHQNLQSQVEQDGRSGHGLRRSSKPYLKEHKALKTLGIIMGTFTLCWLPFFVNI 294
QY 295 VDPFDITYVPGQWTAFLWGLVINGSLNPLFYAFPLNKSFRRAFLIILCCDDERYRPSIL 354
DB 295 VHVQDNILPKVEYILLNMGVYNGAFNPLIYC-RSPDFRIAFQBELLC-----LRSALK 348
QY 355 GQTVPCSTTNGSTHVLDAVECC-GGQWESQ--CH-PPATSPVAAQ---PSDT 402
DB 349 AYVNDSSNS-NGKTDYTGEPNVCHQGEKEBELCEDPPGTEDLVSCPGTVPSDS 403

RESULT 10
Q98841
ID Q98841 PRELIMINARY; PRT; 445 AA.
AC Q98841;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dopamine D1A1 receptor.
GN D1A1.
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97160583; PubMed=9006917;
RA Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Miznik H.B.,
RA Vernier P.;
RT "Early emergence of three dopamine D1 receptor subtypes in
RT vertebrates. Molecular phylogenetic, pharmacological, and functional
RT criteria defining D1A, D1B, and D1C receptors in European eel Anguilla
RT anguilla.";
RL J. Biol. Chem. 272:2778-2787 (1997).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U62918; AAC60067.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS02462; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 445 AA; 49442 MW; 2A36D945DE39ACDD CRC64;

Query Match 27.2%; Score 581; DB 13; Length 445;
Best Local Similarity 36.6%; Pred. No. 3.6e-48;
Matches 131; Conservative 63; Mismatches 124; Indels 40; Gaps 9;

QY 4 LDANVSSERGFSGVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTYFVSLA 63
DB 9 LOGDLPEKD---SSARVLTGCFLLSLIITLTLGNTLVCAAVTRFRHLRSKVTNPFVSLA 65
QY 64 FADLLSVLVMFPFGAIELVDQIWIYGEVFCIVRTSLDVLTTASIFHLCCISLDRIYALC 123
DB 66 ISDLLVAILVMFPKAAATEIVGVFPFGS-FCNIWVAFDVMCSASINLCVLSVDRIYAL- 123
QY 124 CQPLVYRNKMTPLRLALMGCGWVPTFISFLPIMQGNWNIIGIIDLERSLNOGLQD 180
DB 124 SSFPYERKMTKPAFVMSLVAVTSLVLSIFIPVQLNWHKAAAGFPELNGT----- 175
QY 181 FHAIEKRKFNQNSNTYCVFMNKPVAITCSVVAFYIPFLMLVAYRYVYVTAKEHAHQI 240

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DB 176 -----FREPPPPDNCSSLNRTYAISSLSFYIPVAIMIVTYTRIYIAQKQIRRI 227
QY 241 QMLORAGASSESR-----PQADQSHSTRM--RRTKAATLCIIMGCFCLCWAPFFVTNI 294
DB 228 SALERAESAKNRHSNGNSTESSSPKMSFKRTKVLTKLTSVIMGVFVCCWLPFFFLNC 287
QY 295 VDPFDITY-----VPGQWTAFLWGLVINGSLNPLFYAFPLNKSFRRAFLIILCC 343
DB 288 MVYFCEQAPQGAADLPVCSSTTFDVFVWFHANSLSNPIIYAP-NADFRKAFSTLLCC 344

RESULT 11
Q8WND7
ID Q8WND7 PRELIMINARY; PRT; 446 AA.
AC Q8WND7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dopamine 1A receptor.
GN D1AR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX Haegeman A.A., Jacobs K., van Zevenen A., Peelman L.;
RT "Bovine dopamine 1A receptor: cDNA sequence, polymorphisms and
RT mapping.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF381032; AAU37945.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS02462; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 446 AA; 49316 MW; 00F13996BA7CB8EE CRC64;

Query Match 27.2%; Score 580; DB 6; Length 446;
Best Local Similarity 34.4%; Pred. No. 4.6e-48;
Matches 135; Conservative 67; Mismatches 138; Indels 52; Gaps 10;

QY 7 NVSSEEGFGSVE-----KVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTYFV 60
DB 5 NTSMEGTGLVAERDFSRILTACFLSLILLTLGNTLVCAAVTRFRHLRSKVTNPFV 64
QY 61 SLAPADLLSVLVMFPFGAIELVDQIWIYGEVFCIVRTSLDVLTTASIFHLCCISLDRIY 120
DB 65 SLAVSDLLVAVLVMFPKAAAEIAGFPFGS-FCNIWVAFDVMCSASINLCVLSVDRIY 123
QY 121 AICQPLVYRNKMTPLRLALMGCGWVPTFISFLPIMQGNWNIIGIIDLERSLNOGLQD 180
DB 124 AI-SSFPYERKMTKPAAFILISVAVTSLVLSIFIPVQLSWHKAKPTGSPSEGNATSLGT 182
QY 181 FHAIEKRKFNQNSNTYCVFMNKPVAITCSVVAFYIPFLMLVAYRYVYVTAKEHAHQI 240
DB 183 IN-----NCDSSLRTYAISSLSFYIPVAIMIVTYTRIYIAQKQIRRI 228
QY 241 QMLORAGASSE-----SRPQADQSHSTRMRTETKAATLCIIMGCFCLCW 286
DB 229 SALERAAMAAHNCQTTTNGNPNMCECSQPESSFKMSFKR---ETKVLTKLSVIMGVFVCCW 285
QY 287 APFFVTNIVDPFI-----DYTPGVQWTAFLWGLVINGSLNPLFYAFPLNKSFRRAFLII 340

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286 LPFFILNCMVPCGSGETKPCFICDITFDVFWFGWANSNLIPIIYAF-NADFRKAFSTL 344
341 LCCDDERVRPSILGQTPVCSITTTINGSTHVL 372
345 LGC-----YRLCPTTNNAI--ETVSINNGAV 370

RESULT 12
98844 PRELIMINARY; PRT; 448 AA.
Q98844
01-FEB-1997 (TREMBlrel. 02, Created)
01-FEB-1997 (TREMBlrel. 02, Last sequence update)
01-JUN-2003 (TREMBlrel. 24, Last annotation update)
Dopamine D1C receptor.
D1C.
Anguilla anguilla (European freshwater eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
Anguilla.
NCBI_TaxID=7936;
[1]
SEQUENCE FROM N.A.
MEDLINE=97160583; PubMed=9006917;
Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
Vernier P.;
"Early emergence of three dopamine D1 receptor subtypes in
vertebrates. Molecular phylogenetic, pharmacological, and functional
criteria defining DIA, D1B, and D1C receptors in European eel Anguilla
anguilla";
J. Biol. Chem. 272:2778-2787(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; U62921; AAC60068.1; -.
HSSP; P02699; 1F88.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOPOPSN.
PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 448 AA; 50084 MW; OABC0296650B93F3 CRC64;

Query Match 26.7%; Score 569; DB 13; Length 448;
Best Local Similarity 37.9%; Pred. No. 5.5e-47;
Matches 125; Conservative 59; Mismatches 114; Indels 32; Gaps 7;

26 LSTVILMAILGNLWVAVCWDRQLRKIKTNVIVSLAPADLLVSLVMPFGAIELVQDI 85
32 LFLVILSTLGNLTVCAAVIRKFRHLRSKVTNFFVLSLVSDVFLVAVLWPKAVSEVAGY 91
86 WTVGEVFLVRSVLDVLLTASTFHLCCISLDRYYAICQPLVYRNKMTPLRIALMLGQC 145
92 WLFGK-FCTETWIAFDIMCTASILNLCISVDRYWAI-ASPFYERKMTQVAFIMIGVA 149
146 WVIPTFISFLPIMQGNNGIIDLERSLQGLQDPHAIEKRFKNSNSTYCVFVWVKP 205
150 WTLISILSIFPQLNWKH-----AEEDYADD---NSSNHTDCNASLNST 191
206 YAITCSVAFYIPFLMLVAYRIYVYTAKEHAHQIQLORAGASSESRQSDQHSHTRM 265
192 YAISSLISFYIPVIMIGTYTRIYRIAQTQIRRISSLERAEQAQSHQHPDCANENSL 251
266 RT-----ETAAKATCLIMGFCCLCWAPFFVTVNIVDPFID-----YTVPGQVWTAFLWL 314
252 KTFKKEKTVKLTSLIMGVFVFCNLPFFVLCNCPVFCIDIGIDPLCYSDSTFNIFWVF 311
315 GYNSGCLNPFYAFNLKSFRAFLIILCCD 344

312 GWANSSLNPIIYAF-NADFRKAFSTILGCN 340

RESULT 13
98843 PRELIMINARY; PRT; 458 AA.
Q98843
01-FEB-1997 (TREMBlrel. 02, Created)
01-FEB-1997 (TREMBlrel. 02, Last sequence update)
01-JUN-2003 (TREMBlrel. 24, Last annotation update)
Dopamine D1B receptor.
D1B.
Anguilla anguilla (European freshwater eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
Anguilla.
NCBI_TaxID=7936;
[1]
SEQUENCE FROM N.A.
MEDLINE=97160583; PubMed=9006917;
Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
Vernier P.;
"Early emergence of three dopamine D1 receptor subtypes in
vertebrates. Molecular phylogenetic, pharmacological, and functional
criteria defining DIA, D1B, and D1C receptors in European eel Anguilla
anguilla";
J. Biol. Chem. 272:2778-2787(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; U62920; AAC60070.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOPOPSN.
PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 458 AA; 51941 MW; DfSA866F77C6B3E7 CRC64;

Query Match 26.4%; Score 564; DB 13; Length 458;
Best Local Similarity 35.4%; Pred. No. 1.7e-46;
Matches 141; Conservative 63; Mismatches 148; Indels 46; Gaps 12;

9 SSEGFGSGVEKVVLLT---FLSTVILMAILGNLWVAVCWDRQLRKIKTNVIVSLAPA 65
30 SAEKTDGKKEHIVRTVTCGLSLSLILTLGNLILVCSAVLKFRLHRLTKVTNIFIVSLAVS 89
66 DLLVSLVMPFGAIELVQDIWTVGEVFLVRSVLDVLLTASTFHLCCISLDRYYAICQ 125
90 DLFAVLWPKAVSEVAGYDFGP-FCNIWVAFDIMCTASILNLCISVDRYWAI-SS 147
126 PLVYRNKMTPLRIALMLGCGVVIPTFISFLPIMQGNNGIIDLERSLQGLQDPHAIE 185
148 PFYERKMTQVAFIMIGTYTRIYRIAQTQIRRISSLERAEQAQSHQHPDCANENSL 198
186 KRFKNSNSTYCVFVWVKPFAITCSVAFYIPFLMLVAYRIYVYTAKEHAHQIQLOR 245
199 -----GKSENCSSLNREYAISSLSIFYPVAIMIVTVTRIYRIAQTQIRRISSLER 252
246 AGASSES---RQSDQHSHTR--MRTETKAATCLIMGFCCLCWAPFFVTVNIVDPFID 300
253 AAEHAQSCRTNRLSCQHINTLKTSTKRETKVFKTLVIMGVFVCCNLPFFILNCIVPCD 312
301 Y-----TVPGQVWTAFLWGLYNSGCLNPFYAFNLKSFRAFLIILCCDDERVR 350
313 RPTDHTAGLPCVSDTTDFVFWFGWANSNLIPIIYAF-NADFRKAFASLLGCRNFCRSRT 371
351 P-----SILQOTVPCSTTT-----INGSTHVLRDVAV 378
372 PVETVNIISNLVSYNQDTLPHKEIVTAYVNNIPNVVDC 409

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RESULT 14
Q8NEQ8 PRELIMINARY; PRT; 477 AA.
ID Q8NEQ8;
AC Q8NEQ8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dopamine receptor D5.
GN DRD5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S., Guibert B.,
RA Vincent J.D., Niznik H.B., Vernier P.;
RT "The amphioxus D1/beta receptor and the emergence of the vertebrate
RT adrenergic system.";
RL submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ005433; CAA06536.1; --
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 477 AA; 52960 MW; FFB0B7662D368AF2 CRC64;

Query Match 26.4%; Score 563.5; DB 4; Length 477;
Best Local Similarity 34.7%; Pred. No. 28-46;
Matches 137; Conservative 69; Mismatches 146; Indels 43; Gaps 9;

QY 19 KVVLLTFLSTVILMAILGNLLVMVAVCMWRQLRKIKTNVFIYSLAFADLLVSVLVPFGA 78
Db 40 QVVTACLLTLLIITLGNLVCAIVRSEHLRANNTVFIYSLVSDLPVALLVPWKA 99
QY 79 IELVQDIWYGEVFCVLRSLDVLTLTASIFHLCCISLDRIYAIICQPLVYRNKMTPLRI 138
Db 100 VAEVAGYWPFG-AFCDVWVAFDMCSTASILNLCVISVDYNAI-SRPFRYKRMQFORMA 157
QY 139 ALMLGCGWIPFIISPLIMQGN-----NIGIDLERSLNQLGQDFHAIKPKFNQNS 193
Db 158 LVVGLAWTSLISLIPVOLNHRDQAASGGLDLPNNL-----ANMTFWEEDFWEPDV 212
QY 194 NSTYCVFMVKNKYATCSVAVYIPPLMLVAYRIYVTAKEHAHQIOMLQAGASSER 253
Db 213 NAENCSSLNRYAISSSLSIFYPVAINIVTYRIYAOVIRISLEAAEHAQSC 272
QY 254 POSA-----DQSHTRMRTTAAKTLCTIIMGFCFLCWAPPFTVNIUDDPIDYTPG---- 305
Db 273 RSSACAPDXSRASIKETKVLKTLISVINGVFCVLPFFTLNCWVPFCSGHPGPPAG 332
QY 306 -----QVMTAFNLWYNSGLNPFLYAFNLKSFRAFLIILCCDDERYRPSILGQTPV 359
Db 333 FPCVSETTDFVFWGWNSSLNPIYAF-NADFQKVAQLLGCSSHFCSTPV---ETVN 388
QY 360 CSTTTIN-----GSTHVLRDVCEGQ 381
Db 389 ISNELISYNQDIVFHKIEIAAAYIHMPNAVTPGNR 423

RESULT 15
Q96716 PRELIMINARY; PRT; 391 AA.
ID Q96716
AC Q96716;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dopamine D1/beta receptor.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7740;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S., Guibert B.,
RA Vincent J.D., Niznik H.B., Vernier P.;
RT "The amphioxus D1/beta receptor and the emergence of the vertebrate
RT adrenergic system.";
RL submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ005433; CAA06536.1; --
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 391 AA; 42622 MW; 67A5AD944AFA3FBB CRC64;

Query Match 26.3%; Score 562; DB 5; Length 391;
Best Local Similarity 38.5%; Pred. No. 238-46;
Matches 135; Conservative 57; Mismatches 117; Indels 42; Gaps 11;

QY 4 LDANVSSEEGFGS-----VEKVV-LITFLSTVILMAILGNLLVMVAVCMWRQLRK 52
Db 16 LTAN-STEASVGSFAPNPYSAGVAVGLITVI--LILTVIGNVLIVLAVTCHRMRT 72
QY 53 IKTNYFIYSLAFADLLVSVLVPFGAIELVQDIWYGEVFCVLRSLDVLTLTASIFHL 112
Db 73 V-TNFFIVSLACADLSVGLTVLPFAATNDILGYWPFGG-YCDVWVSPDLNSTASILNV 130
QY 113 CISLDRIYAIICQPLVYRNKMTPLRIALMLGCGWIPFIISPLIMQGNNGIIDLERS 172
Db 131 VIAFDRLAITA-PFTYHTRMRTTAAKTLCTIIMGFCFLCWAPPFTV 178
QY 173 LNQGLGQDFHAIKPKFNQNSNTYCVFMVKNKYATCSVAVYIPPLMLVAYRIYV 232
Db 179 YRNQSEALAI-----YSDPCLCIFTASTATIVSSLSIFPLIMLVFYGIFKA 231
QY 233 AKEHAHQIOMLQAGASSERPOSDQSHTRMRTTAAKTLCTIIMGFCFLCWAPPFTV 292
Db 232 ARDQARKINALEGRLEQENNRKKIS-----LAKKEKAARTLGIINGVFLCWLPFFW 285
QY 293 NIVDPFDYTPGVQVMTAFNLWYNSGLNPFLYAFNLKSFRAFLIILCC 343
Db 286 NIVNPFCDRCVQPAVFIATLWLGWINSFAPITIIYAF-NKEFRKVFVVMICC 335

Search completed: August 5, 2004, 13:36:08
Job time : 41 secs
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